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OM protein - protein search, using sw model

Run on: October 5, 2004, 18:50:04 ; Search time 33.2533 Seconds
(without alignments)
1232.039 Million cell updates/sec

Title: US-09-830-321A-1
Perfect score: 852
Sequence: 1 MELALLGLVWAGVIPIQG.....YQKRLRFYWRPHCRGQTGPGC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	852	100.0	145	3 AAB03627	Aab03627 Human pho
2	852	100.0	145	3 AAB12537	Aab12537 Human sec
3	852	100.0	145	4 AAM24100	Aam24100 Human EST
4	852	100.0	145	4 AAE11924	Aae11924 Human CG9
5	852	100.0	150	4 AAM25827	Aam25827 Human pro
6	846	99.3	145	4 AAU09096	Aau09096 Novel hum
7	846	99.3	145	6 ABR44234	Abr44234 Human can
8	846	99.3	145	6 ABR58706	Abr58706 Human can
9	846	99.3	145	6 ABU63124	Abu63124 Human gro
10	624.5	73.3	144	3 AAB12536	Aab12536 Mouse sec
11	624.5	73.3	144	3 AAB11994	Aab11994 Mouse sec
12	500.5	58.7	116	3 AAB24434	Aab24434 Human PRO
13	500.5	58.7	116	3 AAY99450	Aay99450 Human PRO
14	500.5	58.7	116	4 AAU12438	Aau12438 Human PRO
15	500.5	58.7	116	4 AAB66199	Aab66199 Protein o
16	500.5	58.7	116	6 ABO17882	Abol17882 Novel hum
17	500.5	58.7	116	6 ABU81136	Abu81136 Human PRO
18	500.5	58.7	116	6 ABU66836	Abu66836 Human PRO
19	500.5	58.7	116	6 ABUS9917	Abus9917 Novel sec
20	500.5	58.7	116	6 ABO25107	Abol25107 Human sec
21	500.5	58.7	116	6 ABU67112	Abu67112 Human sec
22	500.5	58.7	116	6 ADA46053	Ada46053 Novel hum
23	500.5	58.7	116	6 ADA76484	Ada76484 Human PRO
24	500.5	58.7	116	6 ADA19134	Ada19134 Human PRO
25	500.5	58.7	116	6 ADA61757	Ada61757 Homo sapi

ALIGNMENTS

RESULT 1

AAB03627	ID	AAB03627	standard; protein; 145 AA.
XX	AC	AAB03627;	
XX	DT	05-OCT-2000	(first entry)
XX	DE	Human phospholipase 1 HPPL1.	
XX	XX		
KW	Human; phospholipase 1; HPPL1; cancer; autoimmune disorder; inflammatory disorder; reproductive disorder; infection.		
KW	Human; phospholipase 1; HPPL1; cancer; autoimmune disorder; inflammatory disorder; reproductive disorder; infection.		
XX	OS	Homo sapiens.	
XX	XX		
FH	Key	Location/Qualifiers	
FT	Peptide	1..21	
FT	Peptide	/label= putative_signal_peptide	
FT	Peptide	1..16	
FT	Protein	/label= putative_signal_peptide	
FT	Protein	17..145	
FT	Active-site	/label= putative_mature_HPPL1	
FT	Protein	21..145	
FT	Protein	/label= phospholipase_A2_active_site_signature	
FT	Modified-site	22..145	
FT	Region	/label= putative_mature_HPPL1	
FT	Region	33	
FT	Region	/label= potential_phosphorylation_site	
FT	Region	44..92	
FT	Region	88..140	
FT	Modified-site	/label= active_site_histidine_region	
FT	Modified-site	89	
FT	Modified-site	/label= active_site_aspartic_acid_region	
FT	Modified-site	98	
FT	Modified-site	/label= potential_glycosylation_site	
FT	Modified-site	102	
FT	Modified-site	/label= potential_phosphorylation_site	
XX	WO200024911-A2.		
XX	04-MAY-2000.		
XX	27-OCT-1999;	99WO-US025021.	
XX	27-OCT-1998;	98US-00181317.	
XX	21-JAN-1999;	99US-00234726.	

26	500.5	58.7	116	6	ADB19542	Novel hum
27	500.5	58.7	116	6	ADB28083	Human PRO
28	500.5	58.7	116	6	ADA86562	Novel hum
29	500.5	58.7	116	6	ADB16126	Human PRO
30	500.5	58.7	116	6	ADA47912	Human PRO
31	500.5	58.7	116	6	ABO33692	Novel hum
32	500.5	58.7	116	6	ADA67707	Human PRO
33	500.5	58.7	116	6	ADB30714	Human PRO
34	500.5	58.7	116	6	ADA86010	Novel hum
35	500.5	58.7	116	6	ADA97222	Human PRO
36	500.5	58.7	116	6	ADA79526	Human PRO
37	500.5	58.7	116	6	ADA87665	Novel hum
38	500.5	58.7	116	6	ADB16867	Human PRO
39	500.5	58.7	116	6	ADA91959	Novel hum
40	500.5	58.7	116	6	ADB15022	Human PRO
41	500.5	58.7	116	6	ADB18983	Novel hum
42	500.5	58.7	116	6	ADA94198	Human PRO
43	500.5	58.7	116	6	ADB20094	Novel hum
44	500.5	58.7	116	6	ADB13406	Human PRO
45	500.5	58.7	116	6	ABO43415	Novel hum

PA (INCY-) INCYTE PHARM INC.
 XX Hillman JL, Bandman O, Guesler KJ, Corley NC, Baughn MR;
 PI Azimzai Y, Lal P, Lu DAM;
 XX WPI; 2000-350750/30.
 DR N-PSDB; AAA53269.
 XX Human phospholipase genes and proteins useful to diagnose, prevent or
 PT treat cancer, autoimmune or inflammatory or reproductive disorders.
 XX Claim 1; Page 70-71; 80pp; English.
 XX The present sequence is human phospholipase 1 (HPL1). This protein is
 CC involved in the hydrolysis of membrane phospholipids. The protein and its
 CC coding sequence can be used to diagnose and treat the following: cancers
 CC such as prostate, breast and testicular cancers, autoimmune and
 CC inflammatory disorders such as AIDS, allergies, anaemia, asthma,
 CC atherosclerosis, Crohn's disease, diabetes mellitus, emphysema, Graves'
 CC disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis,
 CC psoriasis, rheumatoid arthritis and systemic lupus erythematosus,
 CC infection caused by viruses, fungi, bacteria, parasites and protozoa, and
 CC reproductive disorders including infertility, disruptions of the
 CC menstrual cycle, polycystic ovary syndrome, ectopic pregnancies,
 CC disruptions of spermatogenesis, cancers within the reproductive tract and
 CC impotence
 XX SQ Sequence 145 AA;
 Query Match 100.0%; Score 852; DB 3; Length 145;
 Best Local Similarity 100.0%; Pred. No. 7e-77;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MELALLCGLVVMAGVPIQGGILNLNMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
 DB 1 MELALLCGLVVMAGVPIQGGILNLNMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
 QY 61 DWCCQTHDCCYDHLTKQCGGIYKDYRYNFSQGNHCSDKGSWCCEQQLCACDKEVAFCLK 120
 DB 61 DWCCQTHDCCYDHLTKQCGGIYKDYRYNFSQGNHCSDKGSWCCEQQLCACDKEVAFCLK 120
 QY 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
 DB 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
 RESULT 2
 AAB12537
 ID AAB12537 standard; protein; 145 AA.
 XX AAB12537;
 AC AAB12537;
 XX 02-NOV-2000 (first entry)
 DT Human secretory phospholipase A2 protein sequence SEQ ID NO:27.
 DE Secretory phospholipase A2; PLA2; anti-allergic; anti-inflammatory;
 XX antibacterial; immunosuppressive; tranquilizer; vulnery; anti-rheumatic;
 KW antithrombotic; septic shock; trauma; pancreatitis; allergic rhinitis;
 KW chronic rheumatoid arthritis.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..10
 FT /label= signal
 FT Protein 21..145
 FT /label= PLA2
 XX WO200034486-A1.
 PN 15-JUN-2000.
 XX

PF 07-DEC-1999; 99WO-JP006844.
 XX 09-DEC-1998; 98JP-00349608.
 XX (SHIO) SHIONOGI & CO LTD.
 PA Ishizaki J, Suzuki N, Hanasaki K;
 XX WPI; 2000-423429/36.
 DR N-PSDB; AAA60878.
 XX Human secretory phospholipase A2 (PLA2) and its encoded gene for
 PT diagnosis and treatment of secretory PLA2-associated diseases e.g. septic
 PT shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid
 PT arthritis.
 XX Claim 1; Page 41; 45pp; Japanese.
 XX The present invention describes human secretory phospholipase A2 (PLA2).
 CC PLA2 has anti-allergic, anti-inflammatory, antibacterial, tranquilizer,
 CC immunosuppressive, vulnery, anti-rheumatic and antiarthritic activities.
 CC Human secretory phospholipase A2 (PLA2), the gene encoding it and
 CC antibodies against it are useful for the diagnosis and treatment of
 CC secretory PLA2-associated diseases e.g. septic shock, trauma,
 CC pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
 CC present sequence represents human PLA2
 XX SQ Sequence 145 AA;
 Query Match 100.0%; Score 852; DB 3; Length 145;
 Best Local Similarity 100.0%; Pred. No. 7e-77;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MELALLCGLVVMAGVPIQGGILNLNMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
 DB 1 MELALLCGLVVMAGVPIQGGILNLNMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
 QY 61 DWCCQTHDCCYDHLTKQCGGIYKDYRYNFSQGNHCSDKGSWCCEQQLCACDKEVAFCLK 120
 DB 61 DWCCQTHDCCYDHLTKQCGGIYKDYRYNFSQGNHCSDKGSWCCEQQLCACDKEVAFCLK 120
 QY 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
 DB 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
 RESULT 3
 AAM24100
 ID AAM24100 standard; protein; 145 AA.
 XX AAM24100;
 AC AAM24100;
 XX 12-OCT-2001 (first entry)
 DT Human EST encoded protein SEQ ID NO: 1625.
 DE Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 KW gene therapy; nutrition.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200154477-A2.
 XX 02-AUG-2001.
 PD 25-JAN-2001; 2001WO-US002687.
 PF 25-JAN-2000; 2000US-00491404.
 XX 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-00663870.
 PR


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XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX PI Cao Y, Drmanac RA, Zhang J, Wehrman T;
XX PI WPI; 2001-476164/51.
XX DR N-PSDB; AAH98759.
XX XX
XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX PT antibodies and research use.
XX PS Claim 20; Page 1102; 1275pp; English.
XX CC
XX CC The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,
XX CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX CC from the organism of interest. They can be used in diagnostics,
XX CC forensics, gene mapping, identification of mutations, to assess
XX CC biodiversity and for nutritional purposes. The present sequence is a
XX CC protein of the invention
XX SQ
XX Sequence 145 AA;
XX Query Match 100.0%; Score 852; DB 4; Length 145;
XX Best Local Similarity 100.0%; Pred. No. 7e-77;
XX Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MELALLGLVVMAGVPIQGGILNLNKKVQVTKMPILSYWPGCHGLGGRQPKDAT 60
Db 1 MELALLGLVVMAGVPIQGGILNLNKKVQVTKMPILSYWPGCHGLGGRQPKDAT 60
Qy 61 DWCCQTHDCCVDHLKTCQGGYKDYRYNFSQGNHCSGKSWCEQQLCACDKEVAFCLK 120
Db 61 DWCCQTHDCCVDHLKTCQGGYKDYRYNFSQGNHCSGKSWCEQQLCACDKEVAFCLK 120
Qy 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
Db 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
RESULT 4
AAE11924
ID AAE11924 standard; protein; 145 AA.
AC AAE11924;
XX DT 18-DEC-2001 (first entry)
XX DE Human CG95 (or C870) lipase protein.
XX KW Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina;
XX KW cardiovascular disease; lipid metabolism; myocardial infarction;
XX KW cerebral ischaemia; arterial thrombosis; thrombolytic; antilipaeamic;
XX KW coronary artery thrombosis; cerebral artery thrombosis; stroke;
XX KW intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
XX KW neuroprotectant; cerebroprotective.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT /label= Signal_peptide
XX FT Domain 21..145
XX FT /note= "Phospholipase A2 domain"
XX FT Protein 25..145
XX FT /note= "Human mature CG95 (or C870) protein"
XX PN WO200179446-A2.
XX PD 25-OCT-2001.
XX XX

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PF 16-APR-2001; 2001WO-US012529.
XX 14-APR-2000; 2000US-0197137P.
XX 20-JUN-2000; 2000US-00598042.
XX 03-AUG-2000; 2000US-00631451.
XX 22-SEP-2000; 2000US-00667298.
XX 17-NOV-2000; 2000US-00714936.
XX (HYSE-) HYSEQ INC.
XX Ballinger DG, Loeb D, Montgomery JR, Tang TY, Zhou P, Goodrich R;
XX Liu C, Asundi V, Zhao QA, Wehrman T, Drmanac RT, Ren F, Qian XB;
XX Wang D;
XX WPI; 2001-611724/70.
XX N-PSDB; AAD19218.
XX Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein
XX receptor polypeptides, useful for preventing diagnosing and treating
XX lipid metabolism disorders, thrombosis and cardiovascular diseases.
XX Claim 10; Fig 1; 266pp; English.
XX The invention relates to polynucleotides encoding proteins CG122, CG179,
XX CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins
XX involved in lipid metabolism and cardiovascular disease such as human
XX apolipoproteins, lipases and lipoprotein receptor proteins. These DNA and
XX protein sequences are useful for treating or preventing disorders
XX associated with apolipoproteins, lipases and lipoprotein receptor (ALLr)
XX expression and for treating lipid metabolism, cardiovascular diseases and
XX thrombosis. Antibodies against these proteins are useful for determining
XX the presence of or predisposition to a disease associated with altered
XX levels of these sequences. ALLr polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them and cells
XX expressing ALLr proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of this polypeptide. Vectors comprising these
XX DNA and protein sequences are also useful for producing ALLr proteins.
XX The nucleic acids and polypeptides of the invention are also useful for
XX the treatment of occlusive cardiovascular diseases, myocardial
XX infarction, cerebral ischaemia, angina, arterial thrombosis, coronary
XX artery thrombosis and cerebral artery thrombosis or intracardiac
XX thrombosis and stroke. The nucleotides of the invention are used in gene
XX therapy. The present sequence is human CG95 (or C870) lipase protein
XX Sequence 145 AA;
XX Query Match 100.0%; Score 852; DB 4; Length 145;
XX Best Local Similarity 100.0%; Pred. No. 7e-77;
XX Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MELALLGLVVMAGVPIQGGILNLNKKVQVTKMPILSYWPGCHGLGGRQPKDAT 60
Db 1 MELALLGLVVMAGVPIQGGILNLNKKVQVTKMPILSYWPGCHGLGGRQPKDAT 60
Qy 61 DWCCQTHDCCVDHLKTCQGGYKDYRYNFSQGNHCSGKSWCEQQLCACDKEVAFCLK 120
Db 61 DWCCQTHDCCVDHLKTCQGGYKDYRYNFSQGNHCSGKSWCEQQLCACDKEVAFCLK 120
Qy 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
Db 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
RESULT 5
AAM25827
ID AAM25827 standard; protein; 150 AA.
XX AC AAM25827;
XX DT 16-OCT-2001 (first entry)
XX DE Human protein sequence SEQ ID NO:1342.

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XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
 KW antiagregant; haemostatic; vulnerary; antitumor; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder.
 XX Homo sapiens.
 XX WO200153455-A2.
 XX 26-JUL-2001.
 XX 22-DEC-2000; 2000WO-US035017.
 XX 23-DEC-1999; 99US-00471275.
 XX 21-JAN-2000; 2000US-00488725.
 XX 25-APR-2000; 2000US-0052317.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-457603/49.
 XX N-PSDB; AAH99768.
 XX Isolated human polynucleotides encoding polypeptides, useful for the
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
 XX Claim 20; Page 278; 1217pp; English.
 XX AAH99166 to AAH99904 encode the human proteins given in AA25225 to
 CC AA25963. The proteins can have activities based on the tissues and cells
 CC they are expressed in, such as: anti-inflammatory; antirheumatic;
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary;
 CC antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders
 XX Sequence 150 AA;

Query Match 100.0%; Score 852; DB 4; Length 150;
 Best Local Similarity 100.0%; Pred. No. 7.3e-77;
 Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MELALLCGLVVMAGVPIQGGILNLMKVKQVTGKMPILSYWPGCHGCGRQPKDAT 60
 DB 6 MELALLCGLVVMAGVPIQGGILNLMKVKQVTGKMPILSYWPGCHGCGRQPKDAT 65

QY 61 DWCCQTHDCYDHLKTCGCGIYKDYRYNFSQGNHCSKGSWCEQQLCACDKEVAFCLK 120
 DB 66 DWCCQTHDCYDHLKTCGCGIYKDYRYNFSQGNHCSKGSWCEQQLCACDKEVAFCLK 125
 QY 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
 DB 126 RNLDYQKRLRFYWRPHCRGQTGPGC 150
 RESULT 6
 AAU09096
 ID AAU09096 standard; protein; 145 AA.
 XX AAU09096;
 AC AAU09096;
 XX 20-DEC-2001 (first entry)
 DT Novel human protein NHP #5.
 DE Human; novel human protein; NHP; antidiabetic; antirheumatic;
 XX antiarthritic; cytostatic; antiarteriosclerotic; vulnerary;
 KW neuroprotective; nootropic; antiparkinsonian;
 KW anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;
 KW hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant;
 KW antitmanic; immunosuppressive; cerebroprotective; antimicrobial;
 KW antiinflammatory; antibacterial; antipsoriatic; thymimetic;
 KW immunomodulator; antiseborrheic; dermatological; vasoconstriction;
 KW gastrointestinal disorder; cardiovascular disorder; hypertension;
 KW coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
 KW cachexia; male infertility; impotence; testicular cancer; lung tumour;
 KW hyperproliferative disorder; pulmonary system disorder;
 KW central nervous system disorder; bone disorder;
 KW neurodegenerative disease; Alzheimer's disease; dementia; paranoia;
 KW Huntington's disease; schizophrenia; mania; dementia; parkinson's disease;
 KW panic disorder; learning disability; amyotrophic lateral sclerosis;
 KW psychosis; autism; sleep disorder; immune system disorder;
 KW Hashimoto's thyroiditis; musculo-skeletal system disorders;
 KW multiple sclerosis; ischaemic brain injury; stroke; infectious disease;
 KW diabetes mellitus; immunological disorder; asthma; AIDS; immunogen;
 KW acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis;
 KW inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;
 KW neural system disorder; respiratory disorder; olfactory disorder;
 KW wound healing.
 XX Homo sapiens.
 PH Key Location/Qualifiers
 FT Region 52..65 /label= Immunogenic_epitope
 FT Region 67..78 /label= Immunogenic_epitope
 FT Region 87..105 /label= Immunogenic_epitope
 FT Region 121..129 /label= Immunogenic_epitope
 FT Region 136..141 /label= Immunogenic_epitope
 FT Region 141..141 /label= Immunogenic_epitope
 XX WO200174896-A1.
 XX 11-OCT-2001.
 XX 02-APR-2001; 2001WO-US010542.
 XX 03-APR-2000; 2000US-0194118P.
 XX 29-SEP-2000; 2000US-0236384P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Moore PA, Ni J, Soppet DR, Coleman TA, Gentz RL, Endress GA;
 PI Li Y, Dillion PU;
 XX WPI; 2001-626394/72.

DR N-PSDB; AAS14884.
XX New human proteins, useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cardiovascular
XX disorders, autoimmune disorders and reproductive disorders.
XX Claim 11; Page 306-307; 318pp; English.
XX
XX The invention relates to novel human proteins (NHP) and the nucleic acids
CC that encode them and antibodies raised against them. The proteins,
CC antibodies and nucleic acids are useful in the diagnosis, prognosis,
CC prevention and/or treatment of diseases and/or disorders involving
CC vasoconstriction, gastrointestinal disorders, cardiovascular disorders
CC (e.g. hypertension, erectile dysfunction, high blood pressure, coronary
CC heart disease and arteriosclerosis), anorexia, obesity, bulimia,
CC cachexia, disorders of small intestine, disorders of reproductive system
CC (e.g. male infertility and/or impotence), testicular cancer, lung tumours
CC and other hyperproliferative disorders, disorders of pulmonary system,
CC central nervous system disorders, bone disorders, neurodegenerative
CC diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's
CC disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,
CC panic disorder, learning disabilities, amyotrophic lateral sclerosis,
CC psychoses, autism, sleep disorders), immune system disorders (e.g.
CC Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,
CC central nervous system disorders (e.g. multiple sclerosis, ischaemic
CC brain injury and/or stroke), infectious diseases, diabetes mellitus,
CC immunological disorders (e.g. asthma, acquired immunodeficient syndrome
CC (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,
CC sepsis, acne, psoriasis and lupus erythematosus), neural system
CC disorders, respiratory disorders, olfactory disorders and wound healing.
XX The present sequence represents an NHP of the invention
SQ Sequence 145 AA;

Query Match 99.3%; Score 846; DB 4; Length 145;
Best Local Similarity 99.3%; Pred. No. 2.8e-76;
Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MELALLGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGGLGGRGPKDAT 60
Db 1 MELALLGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGGLGGRGPKDAT 60

Qy 61 DWCCQTHDCCYDHLTKTQCGSIYKDYRYNFSQGNHCSDKGSWCBOQLCADCKEVAFCLK 120
Db 61 DWCCQTHDCCYDHLTKTQCGSIYKDYRYNFSQGNHCSDKGSWCBOQLCADCKEVAFCLK 120

Qy 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
Db 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145

RESULT 7
ABR44234
ID ABR44234 standard; protein; 145 AA.
XX
AC ABR44234;
XX
DT 18-AUG-2003 (first entry)
XX
DE Human secreted group IID phospholipase A2 (sPLA2) enzyme.
XX
KW Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human;
KW phosphatidylcholine; antibacterial; virucide; cytostatic; vasotropic;
KW antiinflammatory; vulnary; cardiant; chromosome lp35; transgenic;
KW enzyme.
XX
OS Homo sapiens.
XX
PN WO2003033689-A1.
XX
PD 24-APR-2003.
XX
PF 12-OCT-2001; 2001WO-IB002407.

XX 12-OCT-2001; 2001WO-IB002407.
PR (CNRS) CNRS CENT NAT RECH SCI.
XX
PA Lazdunski M, Lambeau G, Valentin E;
XX
FI WPI; 2003-403216/38.
XX
DR Novel mammalian secreted group IIF secreted phospholipase A2, useful for
XX preventing and treating bacterial and viral infections, and cancers.
PT Disclosure; Fig 1; 33pp; English.
XX
XX The invention relates to a mammalian secreted group IIF secreted
CC phospholipase A2 (sPLA2) (I), where the enzyme is Ca²⁺ dependent,
CC maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus
CC phosphatidylcholine with a 15-fold preference. A pharmaceutical
CC composition comprising (I) is useful for treating or preventing viral and
CC bacterial infections, and cancers. A pharmaceutical composition
CC containing compounds capable of inhibiting catalytic activity of (I),
CC biologically active compounds that bind sPLA₂ receptors, or a compound
CC that modulates cell proliferation, cell migration, cell contraction or
CC apoptosis is useful for treating disease states or disorders involving
CC group IIF sPLA₂, such as inflammatory disease, cancers, cardiac and brain
CC ischaemia, acute lung injury, acute respiratory distress syndrome or
CC Crohn's disease. Specific antibodies are useful for searching new
CC secreted mammalian group IIF sPLA₂ or the homologues of the enzyme in
CC other mammals. The encoding polynucleotides and vectors are useful for
CC transforming animals and establishing a line of transgenic animals.
CC Sequences ABR44232-238 represent various human secreted sPLA₂ enzymes
CC used in alignment studies with the GIIF sPLA₂ enzyme
XX
SQ Sequence 145 AA;

Query Match 99.3%; Score 846; DB 6; Length 145;
Best Local Similarity 99.3%; Pred. No. 2.8e-76;
Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MELALLGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGGLGGRGPKDAT 60
Db 1 MELALLGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGGLGGRGPKDAT 60

Qy 61 DWCCQTHDCCYDHLTKTQCGSIYKDYRYNFSQGNHCSDKGSWCBOQLCADCKEVAFCLK 120
Db 61 DWCCQTHDCCYDHLTKTQCGSIYKDYRYNFSQGNHCSDKGSWCBOQLCADCKEVAFCLK 120

Qy 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145
Db 121 RNLDYQKRLRFYWRPHCRGQTGPGC 145

RESULT 8
ABR58706
ID ABR58706 standard; protein; 145 AA.
XX
AC ABR58706;
XX
DT 09-JUL-2003 (first entry)
XX
DE Human cancer related protein SEQ ID NO:363.
XX
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
PN WO2003025138-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-US029560.
XX

PR 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX XX
XX AFAR D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX Zlotnik A;
XX WPI; 2003-354600/33.
XX N-PSDB; ACC72857.
XX
XX New genes that are up-regulated or down-regulated in cancers, useful as
XX PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX PT therapeutic targets for screening drugs for treating these diseases.
XX XX
XX Claim 12; Page 763; 767pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule, which
XX comprises the sequence of any of the genes that are up-regulated or down-
XX regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX related gene nucleotide sequences which encode the proteins given in
XX ABR58521 to ABR58709. Also described: (1) determining the presence or
XX absence of a pathological cell in a patient; (2) an expression vector
XX comprising a nucleic acid molecule described above; (3) a host cell
XX comprising the vector; (4) an isolated polypeptide, which is encoded by
XX the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX of (4); (6) specifically targeting a compound to a pathological cell in a
XX patient by administering to the patient the antibody above; and (7) a
XX drug screening assay. The nucleic acid is useful as diagnostic markers or
XX therapeutic targets. In particular, the nucleic acid is useful for
XX diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX atherosclerosis and endometriosis. The nucleic acid is also useful in
XX drug screening, particularly for identifying agents for treating these
XX pathologies
XX XX
XX SQ Sequence 145 AA;
Query Match 99.3%; Score 846; DB 6; Length 145;
Best Local Similarity 99.3%; Pred. No. 2.8e-76;
Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MELALLGLVVMAGVPIQGGILNLNMVKVQVTGKMPILSYWPGYCHGGLGGRGQPKDAT 60
Db 1 MELALLGLVVMAGVPIQGGILNLNMVKVQVTGKMPILSYWPGYCHGGLGGRGQPKDAT 60
Qy 61 DWCCQTHDCCYDHLTKTQCGSIYKDYRYNFSQGNHCSDKGSWCEQQLCACDKEVAFCLK 120
Db 61 DWCCQTHDCCYDHLTKTQCGSIYKDYRYNFSQGNHCSDKGSWCEQQLCACDKEVAFCLK 120
Qy 121 RNLDYQKRLRFYWRPHCRGQTGTC 145
Db 121 RNLDYQKRLRFYWRPHCRGQTGTC 145
RESULT 9
ABU63124
ID ABU63124 standard; protein; 145 AA.
XX AC ABU63124;
XX DT 25-SEP-2003 (first entry)
XX DE Human group IID secreted phospholipase A2.
XX KW Human; group IID secreted phospholipase A2; virucide; antibacterial;
KW cytostatic; antiinflammatory; vasotropic; cerebroprotective; sPLA2;
phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;
viral infection; bacterial infection; cancer; inflammatory disease;
cardiac ischaemia; brain ischaemia; acute lung injury;
acute respiratory distress syndrome; Crohn's disease; enzyme.
Homo sapiens.
US2003073087-A1.
17-APR-2003.
11-OCT-2001; 2001US-00975456.
11-OCT-2000; 2000US-0239491P.
(LAZD/) LAZDUNSKI M.
(LAMB/) LAMBEAU G.
(VALE/) VALENTIN E.
Lazdunski M, Lambeau G, Valentin E;
WPI; 2003-567302/53.
New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful
for treating or preventing viral or bacterial infections, or cancers, or
screening inhibitors of the enzyme for treating e.g. inflammatory
diseases or ischemia.
Disclosure; Fig 1; 16pp; English.
The invention describes a mammalian secreted group IIF phospholipase A2
(sPLA2), which is Ca2+-dependent, maximally active at pH of about 7-8,
and hydrolyses phosphatidylglycerol versus phosphatidylcholine with about
a 15-fold preference. The mammalian secreted group IIF sPLA2 protein or
nucleic acid, or a pharmaceutical composition is useful for treating
and/or preventing viral infections, bacterial infections, or cancers. The
inhibitors of sPLA2 or a composition comprising sPLA2 inhibitors is
useful for treating disease states or disorders involving group IIF
sPLA2, e.g. inflammatory diseases, cancer, cardiac and brain ischaemia,
acute lung injury, acute respiratory distress syndrome, or Crohn's
disease. The enzyme is also useful for screening various chemical
compounds for treating these diseases. This is the amino acid sequence of
human group IID phospholipase A2 used to determine a consensus sequence
for human sPLA2s
SQ Sequence 145 AA;
Query Match 99.3%; Score 846; DB 6; Length 145;
Best Local Similarity 99.3%; Pred. No. 2.8e-76;
Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MELALLGLVVMAGVPIQGGILNLNMVKVQVTGKMPILSYWPGYCHGGLGGRGQPKDAT 60
Db 1 MELALLGLVVMAGVPIQGGILNLNMVKVQVTGKMPILSYWPGYCHGGLGGRGQPKDAT 60
Qy 61 DWCCQTHDCCYDHLTKTQCGSIYKDYRYNFSQGNHCSDKGSWCEQQLCACDKEVAFCLK 120
Db 61 DWCCQTHDCCYDHLTKTQCGSIYKDYRYNFSQGNHCSDKGSWCEQQLCACDKEVAFCLK 120
Qy 121 RNLDYQKRLRFYWRPHCRGQTGTC 145
Db 121 RNLDYQKRLRFYWRPHCRGQTGTC 145
RESULT 10
AAB12536
ID AAB12536 standard; protein; 144 AA.
XX AC AAB12536;
XX DT 02-NOV-2000 (first entry)
XX DE Mouse secretory phospholipase A2 protein sequence SEQ ID NO:14.

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XX Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
KW antibacterial; immunosuppressive; tranquilizer; vulnular; antirheumatic;
KW antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis;
XX chronic rheumatoid arthritis.
XX Mus musculus.
XX OS
XX FH
XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /label= signal
XX FT 20..144
XX FT /label= PLA2
XX PN
XX W0200034486-A1.
XX PD
XX 15-JUN-2000.
XX PF
XX 07-DEC-1999; 99WO-UP006844.
XX PR
XX 09-DEC-1998; 98JP-00349608.
XX PA (SHIO ) SHIONOGI & CO LTD.
XX PI Ishizaki J, Suzuki N, Hanasaki K;
XX DR
XX WPI; 2000-423429/36.
XX N-PSDB; AAA60866.
XX Human secretory phospholipase A2 (PLA2) and its encoded gene for
XX diagnosis and treatment of secretory PLA2-associated diseases e.g. septic
XX shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid
XX arthritis.
XX Example 3; Page 37; 45pp; Japanese.
XX The present invention describes human secretory phospholipase A2 (PLA2).
XX PLA2 has antiallergic, antiinflammatory, antibacterial, tranquilizer,
XX immunosuppressive, vulnular, antirheumatic and antiarthritic activities.
XX Human secretory phospholipase A2 (PLA2), the gene encoding it and
XX antibodies against it are useful for the diagnosis and treatment of
XX secretory PLA2-associated diseases e.g. septic shock, trauma,
XX pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
XX present sequence represents mouse PLA2, which is used in an example from
XX the present invention
XX SQ Sequence 144 AA;
Query Match 73.3%; Score 624.5; DB 3; Length 144;
Best Local Similarity 71.0%; Pred. No. 3.2e-54;
Matches 103; Conservative 14; Mismatches 27; Indels 1; Gaps 1;
QY 1 MELALLCGLVVMAGVPIPIQGGILNLNKMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Db 1 MRLALLCGL-LLAGITATQGGILNLNKMVTHTGKAFSSYWPYCHGCGRGQPKDAT 59
QY 61 DWCCQTHDCCYDHLKTCGCGIYKDYRYNFSQGNHCSDKGSWCEQQLCACDKEVAFCLK 120
Db 60 DWCCQKHGCCVAHLKIDGCKSLTDNYKYSISQGTIQCSNDSWCEBQQLCACDKEVAFCLK 119
QY 121 RNLDYQKRLRFYWRPHCRGQTPGC 145
Db 120 QNLDYSNKRRLRYWPRCKGKTPAC 144
RESULT 11
AAB11994
ID AAB11994 standard; protein; 144 AA.
XX
XX AAB11994;
XX
XX 24-NOV-2000 (first entry)
XX

```

```

DE Mouse secreted phospholipase A2.
XX
KW Secreted phospholipase A2; PLA2; mouse; murine; recombinant production;
KW antibody; diagnosis; drug screening; expressed sequence tag; EST.
XX
OS
XX Mus musculus.
XX FH
XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /note= "Signal peptide"
XX FT 20..144
XX FT /note= "Mouse mature secreted phospholipase A2"
XX PN
XX JP2000166544-A.
XX PD
XX 20-JUN-2000.
XX PF
XX 09-DEC-1998; 98JP-00349602.
XX PR
XX 09-DEC-1998; 98JP-00349602.
XX PA (SHIO ) SHIONOGI & CO LTD.
XX PI WPI; 2000-458171/40.
XX N-PSDB; AAA72076.
XX Mouse secretion type phospholipase A2.
XX Claim 1; Page 10-11; 12pp; Japanese.
XX This sequence represents a mouse secreted phospholipase A2 (secreted
XX PLA2). A cDNA was initially identified in an EST (expressed sequence tag)
XX database, and a fragment (AAA72077) was isolated from cDNA derived from
XX several mouse tissue types using primers AAA72078-A72081. The full
XX length cDNA was generated using primers AAA72082-A72088. The invention
XX relates to the novel secreted PLA2, nucleic acids encoding it, and
XX variants of the protein which retain phospholipase A2 activity. It also
XX encompasses an expression vector and host cells comprising DNA encoding
XX murine secreted PLA2, a method for the recombinant production of the
XX protein, a method of screening potential inhibitors of the protein and
XX the compounds thus identified, and an antibody specific for murine PLA2.
XX The antibody can be used for the diagnosis of a variety of diseases
XX SQ Sequence 144 AA;
Query Match 73.3%; Score 624.5; DB 3; Length 144;
Best Local Similarity 71.0%; Pred. No. 3.2e-54;
Matches 103; Conservative 14; Mismatches 27; Indels 1; Gaps 1;
QY 1 MELALLCGLVVMAGVPIPIQGGILNLNKMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Db 1 MRLALLCGL-LLAGITATQGGILNLNKMVTHTGKAFSSYWPYCHGCGRGQPKDAT 59
QY 61 DWCCQTHDCCYDHLKTCGCGIYKDYRYNFSQGNHCSDKGSWCEQQLCACDKEVAFCLK 120
Db 60 DWCCQKHGCCVAHLKIDGCKSLTDNYKYSISQGTIQCSNDSWCEBQQLCACDKEVAFCLK 119
QY 121 RNLDYQKRLRFYWRPHCRGQTPGC 145
Db 120 QNLDYSNKRRLRYWPRCKGKTPAC 144
RESULT 12
AAB24434
ID AAB24434 standard; protein; 116 AA.
XX
XX AAB24434;
XX
XX 07-NOV-2000 (first entry)
XX
XX Human PRO1561 protein sequence SEQ ID NO:222.
XX
XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;

```

KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine.

OS Homo sapiens.
XX WO2000032221-A2.
XX PD 08-JUN-2000.
XX PF 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1998; 98WO-US025108.
XX PR 16-DEC-1998; 98US-0112850P.
XX PR 12-JAN-1999; 99US-0115554P.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 12-MAR-1999; 99US-0123957P.
XX PR 28-APR-1999; 99US-0131445P.
XX PR 14-MAY-1999; 99US-0134287P.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 20-JUL-1999; 99US-0144758P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 08-SEP-1999; 99WO-US020594.
XX PR 13-SEP-1999; 99WO-US020944.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 15-SEP-1999; 99WO-US021547.
XX PR 05-OCT-1999; 99WO-US023089.
XX PR 29-OCT-1999; 99US-0162506P.

FA (GETH) GENENTECH INC.
XX AShenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX WPI; 2000-412154/35.
DR N-PSDB; AAA77684.

XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating diagnosing a cardiovascular, endothelial or angiogenic
PT disorders in mammals.

XX Claim 72; Fig 94; 315pp; English.
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating diagnosing a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the prevention,
CC treatment and diagnosis of diseases associated with inappropriate PRO
CC expression such as cardiovascular, endothelial or angiogenic disorders in
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC example, the nucleic acids (NAs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO
CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention

XX Sequence 116 AA;
SQ Query Match 58.7%; Score 500.5; DB 3; Length 116;
Best Local Similarity 82.6%; Pred. No. 5.5e-42;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;

Oy 1 MELALLCGLVVMAGVPIQGGILNLNMVKVQVTGKMPILSWPYGCHGLGGRGQPKDAT 60
D6 1 MELALLCGLVVMAGVPIQGGILNLNMVKVQVTGKMPILSWPYGCHGLGGRGQPKDAT 60

Oy 61 DWCCQTHDCCYDHLKTCQCGIYKDN-----NKSSIHCMW-----LSQRYC 100
|||||

Db 61 DWCCQTHDCCYDHLKTCQCGIYKDN-----NKSSIHCMW-----LSQRYC 100
RESULT 13
AAY99450
ID AAY99450 standard; protein; 116 AA.
XX AC AAY99450;
XX DT 08-AUG-2000 (first entry)
XX DE Human PRO1561 (UNQ768) amino acid sequence SEQ ID NO:378.
XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX OS Homo sapiens.
XX FN WO2000012708-A2.
XX PD 09-MAR-2000.
XX PF 01-SEP-1999; 99WO-US020111.
XX PR 01-SEP-1998; 98US-0098716P.
XX PR 01-SEP-1998; 98US-0098749P.
XX PR 01-SEP-1998; 98US-0098750P.
XX PR 02-SEP-1998; 98US-0098803P.
XX PR 02-SEP-1998; 98US-0098821P.
XX PR 02-SEP-1998; 98US-0098843P.
XX PR 09-SEP-1998; 98US-0099536P.
XX PR 09-SEP-1998; 98US-0099596P.
XX PR 09-SEP-1998; 98US-0099598P.
XX PR 09-SEP-1998; 98US-0099602P.
XX PR 09-SEP-1998; 98US-0099642P.
XX PR 10-SEP-1998; 98US-0099741P.
XX PR 10-SEP-1998; 98US-0099754P.
XX PR 10-SEP-1998; 98US-0099763P.
XX PR 10-SEP-1998; 98US-0099792P.
XX PR 10-SEP-1998; 98US-0099808P.
XX PR 10-SEP-1998; 98US-0099812P.
XX PR 10-SEP-1998; 98US-0099815P.
XX PR 10-SEP-1998; 98US-0099816P.
XX PR 15-SEP-1998; 98US-0100385P.
XX PR 15-SEP-1998; 98US-0100388P.
XX PR 15-SEP-1998; 98US-0100390P.
XX PR 16-SEP-1998; 98US-0100584P.
XX PR 16-SEP-1998; 98US-0100627P.
XX PR 16-SEP-1998; 98US-0100661P.
XX PR 16-SEP-1998; 98US-0100662P.
XX PR 16-SEP-1998; 98US-0100664P.
XX PR 17-SEP-1998; 98US-0100683P.
XX PR 17-SEP-1998; 98US-0100684P.
XX PR 17-SEP-1998; 98US-0100710P.
XX PR 17-SEP-1998; 98US-0100711P.
XX PR 17-SEP-1998; 98US-0100919P.
XX PR 17-SEP-1998; 98US-0100930P.
XX PR 18-SEP-1998; 98US-0100848P.
XX PR 18-SEP-1998; 98US-0100849P.
XX PR 18-SEP-1998; 98US-0101014P.
XX PR 18-SEP-1998; 98US-0101068P.
XX PR 18-SEP-1998; 98US-0101071P.
XX PR 22-SEP-1998; 98US-0101279P.
XX PR 23-SEP-1998; 98US-0101471P.
XX PR 23-SEP-1998; 98US-0101472P.
XX PR 23-SEP-1998; 98US-0101477P.
XX PR 23-SEP-1998; 98US-0101479P.
XX PR 24-SEP-1998; 98US-0101738P.
XX PR 24-SEP-1998; 98US-0101741P.
XX PR 24-SEP-1998; 98US-0101743P.

PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102484P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-0103314P.
 PR 07-OCT-1998; 98US-0103315P.
 PR 07-OCT-1998; 98US-0103328P.
 PR 07-OCT-1998; 98US-0103395P.
 PR 07-OCT-1998; 98US-0103396P.
 PR 07-OCT-1998; 98US-0103401P.
 PR 08-OCT-1998; 98US-0103633P.
 PR 08-OCT-1998; 98US-0103678P.
 PR 08-OCT-1998; 98US-0103679P.
 PR 14-OCT-1998; 98US-0103711P.
 PR 14-OCT-1998; 98US-0104257P.
 PR 20-OCT-1998; 98US-0104987P.
 PR 20-OCT-1998; 98US-0105000P.
 PR 20-OCT-1998; 98US-0105002P.
 PR 21-OCT-1998; 98US-0105104P.
 PR 22-OCT-1998; 98US-0105169P.
 PR 22-OCT-1998; 98US-0105266P.
 PR 26-OCT-1998; 98US-0105693P.
 PR 26-OCT-1998; 98US-0105694P.
 PR 27-OCT-1998; 98US-0105807P.
 PR 27-OCT-1998; 98US-0105881P.
 PR 27-OCT-1998; 98US-0105882P.
 PR 27-OCT-1998; 98US-0106062P.
 PR 28-OCT-1998; 98US-0106023P.
 PR 28-OCT-1998; 98US-0106029P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106249P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
 PR 30-OCT-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 10-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.

XX (GETH) GENENTECH INC.
 PA Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 XX WPI; 2000-237871/20.
 XX N-PSDB; AAA37132.
 DR New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.
 XX Claim 12; Fig 222; 773pp; English.
 XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding then have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention
 XX SQ Sequence 116 AA;
 Query Match 58.7%; Score 500.5; DB 3; Length 116;
 Best Local Similarity 82.6%; Pred. No. 5.5e-42;
 Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;
 QY 1 MELALLCGLVWAGVIQGGILNLNKMVKQVTGMPILSYWPGYCHGLGRGQPKDAT 60
 Db 1 MELALLCGLVWAGVIQGGILNLNKMVKQVTGMPILSYWPGYCHGLGRGQPKDAT 60
 QY 61 DWCCQTHDCCYDHLKTCGCGIYKDYRYNFSQGNTHCSDKGSWCQQLC 109
 Db 61 DWCCQTHDCCYDHLKTCGCGIYKDYRYNFSQGNTHCSDKGSWCQQLC 109
 RESULT 14
 AAB66199
 ID AAB66199 standard; protein; 116 AA.
 XX AAB66199;
 AC AAB66199;
 XX AAB66199;
 DT 02-APR-2001 (first entry)
 XX Protein of the invention #111.
 DE Secreted; transmembrane; gene therapy.
 KW Unidentified.
 OS WO200078961-A1.
 PN 28-DEC-2000.
 PD 18-FEB-2000; 2000WO-US004342.
 PF 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI

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PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2001-071395/08.
DR
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
XX
PS Claim 1; Fig 222; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
SQ Sequence 116 AA;
Query Match 58.7%; Score 500.5; DB 4; Length 116;
Best Local Similarity 82.6%; Pred. No. 5.5e-42;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;
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Db 1 MELALLCGLVWVAGVPIQGGILNLNKMVKQVTGKMPILSYWPGYCHGLGGRGPKDAT 60
QY 61 DWCCQTHCCYDHLTKQTGCGIYKDYRYNFSQGNHCSDKGSCWCEQQLC 109
Db 61 DWCCQTHCCYDHLTKQTGCGIYKDN-----NKSSIHCMD----LSQRYC 100
RESULT 15
AAU12438
ID AAU12438 standard; protein; 116 AA.
XX
XX AC AAU12438;
XX
XX DT 24-OCT-2001 (first entry)
XX
XX DE Human PRO1561 polypeptide sequence.
XX
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIa; gene therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO200140466-A2.
XX
XX PD 07-JUN-2001.
XX
XX PF 01-DEC-2000; 2000WO-US032678.
XX
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 02-DEC-1999; 99WO-US028564.
XX PR 02-DEC-1999; 99WO-US028565.
XX PR 09-DEC-1999; 99US-0170262P.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030911.
XX PR 20-DEC-1999; 99WO-US030999.
XX PR 30-DEC-1999; 99WO-US031243.
XX PR 30-DEC-1999; 99WO-US031274.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000277.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US000365.
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PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-408281/43.
DR N-PSDB; AAS21510.
XX
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
XX Claim 12; Fig 534; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIa. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
XX Sequence 116 AA;
Query Match 58.7%; Score 500.5; DB 4; Length 116;
Best Local Similarity 82.6%; Pred. No. 5.5e-42;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;
QY 1 MELALLCGLVWVAGVPIQGGILNLNKMVKQVTGKMPILSYWPGYCHGLGGRGPKDAT 60
Db 1 MELALLCGLVWVAGVPIQGGILNLNKMVKQVTGKMPILSYWPGYCHGLGGRGPKDAT 60
QY 61 DWCCQTHCCYDHLTKQTGCGIYKDYRYNFSQGNHCSDKGSCWCEQQLC 109
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Db 61 DWCCQTHDCYDHLKTQGGIYKDN-----NKSSIHCMD-----LSQRYC 100

Search completed: October 5, 2004, 19:21:29
Job time : 38.2533 secs

is Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 19:10:14 ; Search time 9.08667 Seconds
(without alignments)
823.819 Million cell updates/sec

Title: US-09-830-321A-1

Perfect score: 852

Sequence: 1 MELALLGLVWAGVPIQG.....YOKRLFYWRPHCRGQTGQC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pap.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	401.5	47.1	146	3	US-08-966-317-4
2	401.5	47.1	146	4	US-09-489-770-4
3	400.5	47.0	146	2	US-08-888-497-35
4	400.5	47.0	146	5	US-09-362-230-35
5	400.5	47.0	146	5	PCT-US94-07926-35
6	395.5	46.4	144	1	US-08-186-895-10
7	395.5	46.4	144	2	US-08-888-497-37
8	395.5	46.4	144	4	US-09-362-230-37
9	395.5	46.4	144	5	PCT-US94-07926-37
10	371.5	43.6	146	3	US-08-966-317-3
11	371.5	43.6	146	4	US-09-489-770-3
12	367.5	43.1	124	1	US-08-170-360-4
13	367.5	43.1	124	2	US-08-888-497-39
14	367.5	43.1	124	4	US-09-362-230-39
15	367.5	43.1	124	5	US-09-740-569-2
16	367.5	43.1	124	5	PCT-US94-07926-39
17	360	42.3	125	2	US-08-888-497-42
18	360	42.3	125	4	US-09-362-230-42
19	360	42.3	125	5	PCT-US94-07926-42
20	347	40.7	138	2	US-08-888-497-32
21	347	40.7	138	4	US-09-362-230-32
22	347	40.7	138	5	PCT-US94-07926-32
23	332	39.0	125	1	US-08-170-360-5
24	329.5	38.7	122	1	US-07-734-534A-1
25	328.5	38.6	118	2	US-08-888-497-40
26	328.5	38.6	118	4	US-09-087-094-5
27	328.5	38.6	118	4	US-09-362-230-40

28	328.5	38.6	118	5	PCT-US94-07926-40
29	315.5	37.0	137	2	US-08-888-497-30
30	315.5	37.0	137	4	US-09-362-230-30
31	315.5	37.0	137	5	PCT-US94-07926-30
32	305.5	35.9	117	2	US-08-888-497-44
33	305.5	35.9	117	4	US-09-362-230-44
34	305.5	35.9	117	5	PCT-US94-07926-44
35	295.5	34.7	130	2	US-08-888-497-43
36	295.5	34.7	130	4	US-09-362-230-43
37	295.5	34.7	130	5	PCT-US94-07926-43
38	295.5	34.7	158	4	US-08-888-497-22
39	295.5	34.7	158	5	US-09-362-230-22
40	295.5	34.7	158	5	PCT-US94-07926-22
41	263.5	30.9	165	3	US-08-966-317-1
42	263.5	30.9	165	4	US-09-489-770-1
43	242.5	28.5	148	2	US-08-888-497-36
44	242.5	28.5	148	4	US-09-362-230-36
45	242.5	28.5	148	5	PCT-US94-07926-36

ALIGNMENTS

RESULT 1
US-08-966-317-4
; Sequence 4, Application US/08966317
; Patent No. 6103469
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; NUMBER OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; TITLE OF INVENTION: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,317
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 204319
; US-08-966-317-4

11/7/1997 (Ciling)

Query Match 47.1%; Score 401.5; DB 3; Length 146;
Best Local Similarity 47.9%; Pred. No. 1.1e-34;

	Matches	70; Conservative	23; Mismatches	52; Indels	1; Gaps	
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QY	60	TDWCCCTHDCCYDHLKTKGGCIYKDYRYRNSQNIHCSDKGSWGEQGLPACDKEVAFCL	119			
Db	61	TDWCCVTHDCCYNPLEKRGGKGTKELTKYFSYRGQGISCSITNQDSCKQLCCQDKAAAEFC	120			
QY	120	KRNLDTYQKRLRFVYWRPHCRGQTGCG	145			
Db	121	ARNKKSYSLLKYOFYLNKFKCKGKTSC	146			

RESULT 2
 US-09-489-770-4
 ; Sequence 4, Application US/09489770
 ; Patent No. 639301
 ; GENERAL INFORMATION:
 ; APPLICANT: Hawkins, Phillip R.
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/489,770
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/966,317
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0403 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 146 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 204319
 ; US-09-489-770-4

[illegible]

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Db      61  TDWCCVTHDCYNRLKRGCGTGKFLTYKFSYRGQISCSSTNQDSCRKQLCQCDKAAAEFCF 120
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RESULT 3
US-08-888-497-35
; Sequence 35, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,497
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIORITY APPLICATION NUMBER: US/08/651,405
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-497-35

Query Match 47.0%; Score 400.5; DB 2; Length 146;
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

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Db      1 MKVLLLVAVVIMAFGSIQVGSLLERGMILFKTKREADVSYGYGCHGCGVGRGSPKDA 60
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QY      60  TDWCCCTHDCYDHLTKTQCGGIYKDYRYNFSQNTIHCSDKGSCWCEQOLCACDKEVAFCL 119
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QY      120  KRNLDTYQKELRFYWRPHCRGQTGPGC 145
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Db      121  ARNKA$YSLKYQFYLNKFKCGKGTSC 146

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RESULT 4
US-09-362-230-35
; Sequence 35, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,230
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/888,497
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-362-230-35

Query Match 47.0%; Score 400.5; DB 4; Length 146;
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

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Db 1 MKVLLLLAVVIMAFGSIQVQGSLLLEFGQMILFKTKRADVSYGYFGCHGCGVGRGSPDA 60

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Db 121 ARNKSYSLKYQFYPNKFCCKGKTPSC 146

RESULT 5
PCT-US94-07926-35
; Sequence 35, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.

; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-35

Query Match 47.0%; Score 400.5; DB 5; Length 146;
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

Qy 1 MELALLGLVMA-GVPIQGGILNKNKQVTKMPILSYWPGCHGLGGRGPKDA 59
Db 1 MKVLLLLAVVIMAFGSIQVQGSLLLEFGQMILFKTKRADVSYGYFGCHGCGVGRGSPDA 60

Qy 60 TDWCCQTHDCCYDHLKTOGGGIYKDYRYNFSQNIHCSDKGWCBOQLCACDKEVAFCL 119
Db 61 TDMCCVTHDCCYNLRKRGCGTKFVTYKFSYRGQISCSSTNQDSCKRQQLCQCKAAAEFCF 120

Qy 120 KRNLDITYKRLRFYWRPHCRGQTPGC 145
Db 121 ARNKSYSLKYQFYPNKFCCKGKTPSC 146

RESULT 6
US-08-186-895-10
; Sequence 10, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
; APPLICANT: Hollis, Melvyn
; APPLICANT: Needham, Maurice R.C.
; APPLICANT: Gooding, Clare
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: Expression Systems
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.

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; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,895
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,383
; FILING DATE: 09-APR-1993
; APPLICATION NUMBER: US/07/810,414
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: ENK/3893/93802/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-186-895-10

Query Match 46.4%; Score 395.5; DB 1; Length 144;
Best Local Similarity 47.6%; Pred. No. 4.7e-34;
Matches 69; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

Qy 1 MELALCLGLVVMAGVPIQGGILNLNMVKVQVTGKMPILSYWPGYCHGGLGGRGPKDAT 60
Db 1 MKTELLAVIMIFGLLOAHGNLVNFRHMIKLTGKEAALSYGFYCHGCGVGRGSPKDAT 60

Qy 61 DWCCQTHDCCYDHLKTOCGGIYKDYRYNFSQGNHCSDKGSWCBEQQLCACDKEVAFCLK 120
Db 61 DRCCVTHDCCYKLEKRGCGTKFLSYKFSNNGSRITCAKQDS-CRSQLECDKAAATCFA 119

Qy 121 RNLDTYQKRLRFYWRPHRCGQTGPGC 145
Db 120 RNKTYNKYQYYSNKHCRGSGTPRC 144

RESULT 7
US-08-888-497-37
; Sequence 37, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,230
; FILING DATE:
; CLASSIFICATION:

; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,405
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-497-37

Query Match 46.4%; Score 395.5; DB 2; Length 144;
Best Local Similarity 47.6%; Pred. No. 4.7e-34;
Matches 69; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

Qy 1 MELALCLGLVVMAGVPIQGGILNLNMVKVQVTGKMPILSYWPGYCHGGLGGRGPKDAT 60
Db 1 MKTELLAVIMIFGLLOAHGNLVNFRHMIKLTGKEAALSYGFYCHGCGVGRGSPKDAT 60

Qy 61 DWCCQTHDCCYDHLKTOCGGIYKDYRYNFSQGNHCSDKGSWCBEQQLCACDKEVAFCLK 120
Db 61 DRCCVTHDCCYKLEKRGCGTKFLSYKFSNNGSRITCAKQDS-CRSQLECDKAAATCFA 119

Qy 121 RNLDTYQKRLRFYWRPHRCGQTGPGC 145
Db 120 RNKTYNKYQYYSNKHCRGSGTPRC 144

RESULT 8
US-09-362-230-37
; Sequence 37, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,230
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/888,497
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-37

Query Match 46.4%; Score 395.5; DB 4; Length 144;
Best Local Similarity 47.6%; Pred. No. 4.7e-34;
Matches 69; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

QY 1 MELALLGLVWAGVIPIQGGILNLNMVKVQVTGKMPILSYWPGYCHGGLGGRGPKDAT 60
Db 1 MKTLLAVIMIFGLLQAHGNLVNFRMIKLTGKEAALSIFYGCHGCVGGRGSPKDAT 60

QY 61 DWCCOTHCCDHLTKTQGGIYKYDYRYNFSQNIHCSDKGSCWCEQQLCACDKEVAFCLK 120
Db 61 DRCCVTHDCCYKRLKRGCGTKFLSKFSNSGSRITCAKQDS-CRSQLECDKAAATCFA 119

QY 121 RNLDTYQKRLRFYRPHCRGOTPGC 145
Db 120 RNKITYNKYQYYSNKHCRGSTPRC 144

US-09-830-321a-1.rai
RESULT 9
PCT-US94-07926-37
; Sequence 37, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-37

Query Match 46.4%; Score 395.5; DB 5; Length 144;
Best Local Similarity 47.6%; Pred. No. 4.7e-34;
Matches 69; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

QY 1 MELALLGLVWAGVIPIQGGILNLNMVKVQVTGKMPILSYWPGYCHGGLGGRGPKDAT 60
Db 1 MKTLLAVIMIFGLLQAHGNLVNFRMIKLTGKEAALSIFYGCHGCVGGRGSPKDAT 60

QY 61 DWCCOTHCCDHLTKTQGGIYKYDYRYNFSQNIHCSDKGSCWCEQQLCACDKEVAFCLK 120
Db 61 DRCCVTHDCCYKRLKRGCGTKFLSKFSNSGSRITCAKQDS-CRSQLECDKAAATCFA 119

QY 121 RNLDTYQKRLRFYRPHCRGOTPGC 145
Db 120 RNKITYNKYQYYSNKHCRGSTPRC 144

US-08-966-317-3
; Sequence 3, Application US/08966317
; Patent No. 6103469
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,317
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0403 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
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; LIBRARY: GenBank
; CLONE: 984837
US-08-966-317-3

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Query Match	43.6%;	Score 371.5;	DB 3;	Length 146;
Best Local Similarity	47.3%;	Pred. No. 1.6e-31;		
Matches 69;	Conservative 19;	Mismatches 57;	Indels 1;	Gaps 1;

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120 KRNIDTYQKRLRFYWPHCRGQTGCG 145

Dp
121 ARNKITYSLKYOFYPNMFCKGKKPKC 146

RESULT 11
US-09-489-770-3
; Sequence 3, Application US/09489770
; Patent No. 6399301
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

Query Match	43.6%;	Score 371.5;	DB 4;	Length 146;
Best Local Similarity	47.3%;	Pred. No. 1.6e-31;		
Matches 69;	Conservative	19;	Mismatches 57;	Indels 1;
				Gaps 1;

[illegible]

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	Query Match	43.1%;	Score 367.5;	DB 1;	Length 124;	
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y	22	IILNLKWKQVYTGKMPILLSWYPGYCHGLGGRGPKDATTWCCTHDCCYDHLTKTQGCI	81			
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b	2	LYNFHRMLKLITGKEAALSYFYGYCHGVGGRGFKATDRCCVTHDCCKYELEKRGCGT	61			
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y	82	YKDYYRYNFSQNHCISDKSGWCEQLCACDKEVAFLKRNLDTYQKELRFYWPBPHCRQG	141			
	: :					: :


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RESULT 14
US-09-362-230-39
; Sequence 39, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09362,230
; APPLICATION NUMBER: US/09362,230
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/888,497
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-362-230-39

Query Match      43.1%; Score 367.5; DB 4; Length 124;
Best Local Similarity 51.6%; Pred. No. 3.4e-31;
Matches    64; Conservative   16; Mismatches 43; Indels    1; Gaps    1;

QY      22 ILNLKMWKVQVTGKMPILSYWYPYGHCGHGGRGOPKDATWCCTHCCVYDLTKTQCGI 81
       :: : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      2 LVNFRMIKLTTCKEALSLVGFGCHGVGRGSPKDATRCVVTHCCVKRLERKRGCGT 61
       : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY      82 YKDYYRNFYSQGNIHCSKGDSWCQEQLCACDKEVAFCLEKNLDTYOKRLRPFWPHCRGQ 141
       : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      62 KFLSYKFSNGSGSRITCAKQDS-CRSQCECDKAAATCFARNKTYYNKKYQYYSNKHCRGS 120
       : : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY      142 TPQC 145
Db      121 TPRC 124

RESULT 15
US-09-740-569-2
; Sequence 2, Application US/09740569
; Patent No. 6475484
; GENERAL INFORMATION:

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Result No.	Score	Query Match	Length	DB	ID	Description
1	852	100.0	145	9	US-09-835-996A-6	Sequence 6, Appli
2	852	100.0	150	12	US-10-296-115-1342	Sequence 1342, Ap
3	846	99.3	145	9	US-09-969-384-17	Sequence 17, Appl
4	846	99.3	145	10	US-09-975-456B-7	Sequence 7, Appli
5	500.5	58.7	116	10	US-09-946-374-378	Sequence 378, App
6	500.5	58.7	116	12	US-10-147-493-534	Sequence 534, App
7	500.5	58.7	116	12	US-10-145-127-534	Sequence 534, App
8	500.5	58.7	116	12	US-10-160-503-534	Sequence 534, App
9	500.5	58.7	116	12	US-10-143-118-534	Sequence 534, App
10	500.5	58.7	116	12	US-10-144-993-534	Sequence 534, App
11	500.5	58.7	116	12	US-10-158-787-534	Sequence 534, App
12	500.5	58.7	116	12	US-10-140-024-534	Sequence 534, App
13	500.5	58.7	116	12	US-10-140-808-534	Sequence 534, App
14	500.5	58.7	116	12	US-10-006-485A-378	Sequence 378, App
15	500.5	58.7	116	12	US-10-013-907A-378	Sequence 378, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES

Result No.	Score	Query *			ID	Description
		Match	Length	DB		
1	852	100.0	145	9	US-09-835-996A-6	Sequence 6, Appli
2	852	100.0	150	12	US-10-296-115-1342	Sequence 1342, Ap
3	846	99.3	145	9	US-09-969-384-17	Sequence 17, Appl
4	846	99.3	145	10	US-09-975-456B-7	Sequence 7, Appli
5	500.5	58.7	116	10	US-09-946-374-378	Sequence 378, App
6	500.5	58.7	116	12	US-10-147-493-534	Sequence 534, App
7	500.5	58.7	116	12	US-10-145-127-534	Sequence 534, App
8	500.5	58.7	116	12	US-10-160-503-534	Sequence 534, App
9	500.5	58.7	116	12	US-10-143-118-534	Sequence 534, App
10	500.5	58.7	116	12	US-10-144-993-534	Sequence 534, App
11	500.5	58.7	116	12	US-10-158-787-534	Sequence 534, App
12	500.5	58.7	116	12	US-10-140-024-534	Sequence 534, App
13	500.5	58.7	116	12	US-10-140-808-534	Sequence 534, App
14	500.5	58.7	116	12	US-10-006-485A-378	Sequence 378, App
15	500.5	58.7	116	12	US-10-013-907A-378	Sequence 378, App

ALIGNMENTS

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RESULT 1
US -09-835-996A-6
/ Sequence 6, Application US/09835996A
/ Patent No. US20020142953A1
/ GENERAL INFORMATION:
/ APPLICANT: Ballinger, Dennis
/ APPLICANT: Loeb, Debra
/ APPLICANT: Montgomery, Julie
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhao, Qing
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Dmanac, Radoje
/ APPLICANT: Ren, Feiyang
/ APPLICANT: Qian, Xiaohong
/ APPLICANT: Wang, Dunrui
/ TITLE OF INVENTION: MATERIALS AND METHODS FOR
/ FILE REFERENCE: 28110/35915A
/ CURRENT APPLICATION NUMBER: US/09/835996A
/ PRIOR FILING DATE: 2001-04-16
/ CURRENT APPLICATION NUMBER: US 60/197,744
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/714,147
/ PRIOR FILING DATE: 2000-11-17
/ PRIOR APPLICATION NUMBER: US 09/667,777
/ PRIOR FILING DATE: 2000-09-22
/ PRIOR APPLICATION NUMBER: US 09/631,147
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: US 09/598,888
/ PRIOR FILING DATE: 2000-06-20
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 6
/ LENGTH: 145
/ TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-835-996A-6

Query Match      100.0%; Score 852; DB 9; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.6e-81;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTKMPILSYWPGCHGCGLGGRGQPKDAT 60
DB 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTKMPILSYWPGCHGCGLGGRGQPKDAT 60
QY 61 DWCCQTHDCCYDHLKTQCGGIYKDYRYNFSQGNHCSDKGSWCEQQLCADCDEKVAFCCLK 120
DB 61 DWCCQTHDCCYDHLKTQCGGIYKDYRYNFSQGNHCSDKGSWCEQQLCADCDEKVAFCCLK 120
QY 121 RNLDYQKRLRFYWRPHCRGQTPGC 145
DB 121 RNLDYQKRLRFYWRPHCRGQTPGC 145

RESULT 2
US-10-296-115-1342
; Sequence 1342, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1342
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1342

Query Match      100.0%; Score 852; DB 12; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.6e-81;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTKMPILSYWPGCHGCGLGGRGQPKDAT 60
DB 6 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTKMPILSYWPGCHGCGLGGRGQPKDAT 65
QY 61 DWCCQTHDCCYDHLKTQCGGIYKDYRYNFSQGNHCSDKGSWCEQQLCADCDEKVAFCCLK 120
DB 66 DWCCQTHDCCYDHLKTQCGGIYKDYRYNFSQGNHCSDKGSWCEQQLCADCDEKVAFCCLK 125
QY 121 RNLDYQKRLRFYWRPHCRGQTPGC 145
DB 126 RNLDYQKRLRFYWRPHCRGQTPGC 150

RESULT 3
US-09-969-384-17
; Sequence 17, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT055PI
; CURRENT APPLICATION NUMBER: US/09/969,384
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118

; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 17
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-384-17

Query Match      99.3%; Score 846; DB 9; Length 145;
Best Local Similarity 99.3%; Pred. No. 6.7e-81;
Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTKMPILSYWPGCHGCGLGGRGQPKDAT 60
DB 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTKMPILSYWPGCHGCGLGGRGQPKDAT 60
QY 61 DWCCQTHDCCYDHLKTQCGGIYKDYRYNFSQGNHCSDKGSWCEQQLCADCDEKVAFCCLK 120
DB 61 DWCCQTHDCCYDHLKTQCGSIYKDYRYNFSQGNHCSDKGSWCEQQLCADCDEKVAFCCLK 120
QY 121 RNLDYQKRLRFYWRPHCRGQTPGC 145
DB 121 RNLDYQKRLRFYWRPHCRGQTPGC 145

RESULT 4
US-09-975-456B-7
; Sequence 7, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In version 2.1
; SEQ ID NO 7
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-7

Query Match      99.3%; Score 846; DB 10; Length 145;
Best Local Similarity 99.3%; Pred. No. 6.7e-81;
Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTKMPILSYWPGCHGCGLGGRGQPKDAT 60
DB 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTKMPILSYWPGCHGCGLGGRGQPKDAT 60
QY 61 DWCCQTHDCCYDHLKTQCGGIYKDYRYNFSQGNHCSDKGSWCEQQLCADCDEKVAFCCLK 120
DB 61 DWCCQTHDCCYDHLKTQCGSIYKDYRYNFSQGNHCSDKGSWCEQQLCADCDEKVAFCCLK 120
QY 121 RNLDYQKRLRFYWRPHCRGQTPGC 145
DB 121 RNLDYQKRLRFYWRPHCRGQTPGC 145

RESULT 5
US-09-946-374-378
; Sequence 378, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
```

APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
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PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
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PRIOR APPLICATION NUMBER: 60/100584
PRIOR FILING DATE: 1998-09-16
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PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100683
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100710
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100711
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100849
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101014
PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-22
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PRIOR FILING DATE: 1998-09-29
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PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102484
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102684

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; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
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; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
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; PRIOR APPLICATION NUMBER: 60/103679
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; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match      58.7%; Score 500.5; DB 10; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;

Qy 1 MELALLGLVVMAGVIPIQGGILNLNKKVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Db 1 MELALLGLVVMAGVIPIQGGILNLNKKVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60

Qy 61 DWCCQTHDCCYDHLTKTQGGIYKDYRYNFSQGNHCSDKGSWCEQQLC 109
Db 61 DWCCQTHDCCYDHLTKTQGGIYKDN-----NKSSIHCM-----LSQRYC 100

RESULT 6
US-10-147-493-534
; Sequence 534, Application US/10147493
; Publication No. US2004029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C252
; CURRENT APPLICATION NUMBER: US/10/145,127
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-147-493-534

Query Match      58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;

Qy 1 MELALLGLVVMAGVIPIQGGILNLNKKVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Db 1 MELALLGLVVMAGVIPIQGGILNLNKKVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60

Qy 61 DWCCQTHDCCYDHLTKTQGGIYKDYRYNFSQGNHCSDKGSWCEQQLC 109
Db 61 DWCCQTHDCCYDHLTKTQGGIYKDN-----NKSSIHCM-----LSQRYC 100

RESULT 7
US-10-145-127-534
; Sequence 534, Application US/10145127
; Publication No. US20040033558A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C252
; CURRENT APPLICATION NUMBER: US/10/145,127
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-145-127-534

Query Match      58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;

Qy 1 MELALLGLVVMAGVIPIQGGILNLNKKVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Db 1 MELALLGLVVMAGVIPIQGGILNLNKKVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60

Qy 61 DWCCQTHDCCYDHLTKTQGGIYKDYRYNFSQGNHCSDKGSWCEQQLC 109
Db 61 DWCCQTHDCCYDHLTKTQGGIYKDN-----NKSSIHCM-----LSQRYC 100

RESULT 8
US-10-147-493-534
; Sequence 534, Application US/10147493
; Publication No. US2004029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
```

```
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;

Qy 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Db 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Qy 61 DWCCQTHDCCYDHLTKTQCGGIYKDYRYNFSQGNHCSDKGSWCEQQLC 109
Db 61 DWCCQTHDCCYDHLTKTQCGGIYKDN-----NKSSIHCM-----LSQRYC 100

RESULT 8
US-10-160-503-534
; Sequence 534, Application US/10160503
; Publication No. US20040033559A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C446
; CURRENT APPLICATION NUMBER: US/10/160,503
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-160-503-534

Query Match 58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;

Qy 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Db 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Qy 61 DWCCQTHDCCYDHLTKTQCGGIYKDYRYNFSQGNHCSDKGSWCEQQLC 109
Db 61 DWCCQTHDCCYDHLTKTQCGGIYKDN-----NKSSIHCM-----LSQRYC 100

RESULT 9
US-10-143-118-534
; Sequence 534, Application US/10143118
; Publication No. US20040038335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C261
; CURRENT APPLICATION NUMBER: US/10/144,993
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-144-993-534

Query Match 58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;
```

```
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C228
; CURRENT APPLICATION NUMBER: US/10/143,118
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-118-534

Query Match 58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;

Qy 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Db 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGCGRGQPKDAT 60
Qy 61 DWCCQTHDCCYDHLTKTQCGGIYKDYRYNFSQGNHCSDKGSWCEQQLC 109
Db 61 DWCCQTHDCCYDHLTKTQCGGIYKDN-----NKSSIHCM-----LSQRYC 100

RESULT 10
US-10-144-993-534
; Sequence 534, Application US/10144993
; Publication No. US20040038336A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C261
; CURRENT APPLICATION NUMBER: US/10/144,993
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-144-993-534

Query Match 58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;
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QY 1 METALLCGLVVMAGVIPIQGGILNLNMVKVQVTGKMPILSYWPYCHGCHGLGGRGQPKDAT 60
Db 1 METALLCGLVVMAGVIPIQGGILNLNMVKVQVTGKMPILSYWPYCHGCHGLGGRGQPKDAT 60
QY 61 DWCCQTHDCCYDHLKTQCGGIYKDN-----NKSSIHCMD-----LSQRYC 109
Db 61 DWCCQTHDCCYDHLKTQCGGIYKDN-----NKSSIHCMD-----LSQRYC 100

RESULT 11
US-10-158-787-534
; Sequence 534, Application US/10158787
; Publication No. US20040039164A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C449
; CURRENT APPLICATION NUMBER: US/10/158,787
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-158-787-534

Query Match 58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;
QY 1 METALLCGLVVMAGVIPIQGGILNLNMVKVQVTGKMPILSYWPYCHGCHGLGGRGQPKDAT 60
Db 1 METALLCGLVVMAGVIPIQGGILNLNMVKVQVTGKMPILSYWPYCHGCHGLGGRGQPKDAT 60
QY 61 DWCCQTHDCCYDHLKTQCGGIYKDN-----NKSSIHCMD-----LSQRYC 109

Db 61 DWCCQTHDCCYDHLKTQCGGIYKDN-----NKSSIHCMD-----LSQRYC 100

RESULT 12
US-10-140-024-534
; Sequence 534, Application US/10140024
; Publication No. US20040058424A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C69
; CURRENT APPLICATION NUMBER: US/10/140,024
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-024-534

Query Match 58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;
QY 1 METALLCGLVVMAGVIPIQGGILNLNMVKVQVTGKMPILSYWPYCHGCHGLGGRGQPKDAT 60
Db 1 METALLCGLVVMAGVIPIQGGILNLNMVKVQVTGKMPILSYWPYCHGCHGLGGRGQPKDAT 60
QY 61 DWCCQTHDCCYDHLKTQCGGIYKDN-----NKSSIHCMD-----LSQRYC 109
Db 61 DWCCQTHDCCYDHLKTQCGGIYKDN-----NKSSIHCMD-----LSQRYC 100

RESULT 13
US-10-140-808-534
; Sequence 534, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William


```
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; PRIOR FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 534
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-534

Query Match      58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;

QY 1 METALLCGLVWAGVIPIQGGILNLNMVKQVTGKMPILSYWPGYCHGCGRGQPKDAT 60
Db 1 METALLCGLVWAGVIPIQGGILNLNMVKQVTGKMPILSYWPGYCHGCGRGQPKDAT 60

QY 61 DWCCQTHDCCYDHLTKQGGIYKDYRYNFSQGNHCHSDKGSWCQQLC 109
Db 61 DWCCQTHDCCYDHLTKQGGIYKDN-----NKSIIHCMD-----LSQRYC 100

RESULT 14
US-10-006-485A-378
; Sequence 378, Application US/10006485A
; Publication No. US20030064062A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
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; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
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; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
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;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101741
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101743
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101915
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101916
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;; PRIOR FILING DATE: 1998-09-29
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;; PRIOR FILING DATE: 1998-09-30
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;; PRIOR APPLICATION NUMBER: 60/102571
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102694
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102687
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102965
;; PRIOR FILING DATE: 1998-10-02
;; PRIOR APPLICATION NUMBER: 60/103258
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103314
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103315
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103328
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103395
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103396
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103401
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103449
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103633
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103678
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103679
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103711
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/104257
;; PRIOR FILING DATE: 1998-10-14
;; PRIOR APPLICATION NUMBER: 60/104987
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104
;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26

;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105881
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105882
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/106023
;; PRIOR FILING DATE: 1998-10-28

Query Match 58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;
QY 1 MELALLCGLVVMAGVPIQGGILNLNKMKVQVTGKMPILSYWPGYCHGCGRQPKDAT 60
Db 1 MELALLCGLVVMAGVPIQGGILNLNKMKVQVTGKMPILSYWPGYCHGCGRQPKDAT 60
QY 61 DWCCQTHDCCYDHLKTQCGGIYKDYRYNFSQGNHCHSDKGSWCEQQLC 109
Db 61 DWCCQTHDCCYDHLKTQCGGIYKDN-----NKSIHCMD-----LSQRYC 100

RESULT 15

US-10-013-907A-378
; Sequence 378, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C34
; CURRENT APPLICATION NUMBER: US/10/013,907A
; CURRENT FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 378
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-907A-378

Query Match 58.7%; Score 500.5; DB 12; Length 116;
Best Local Similarity 82.6%; Pred. No. 1.1e-44;
Matches 90; Conservative 4; Mismatches 6; Indels 9; Gaps 2;
QY 1 MELALLCGLVVMAGVPIQGGILNLNKMKVQVTGKMPILSYWPGYCHGCGRQPKDAT 60
Db 1 MELALLCGLVVMAGVPIQGGILNLNKMKVQVTGKMPILSYWPGYCHGCGRQPKDAT 60
QY 61 DWCCQTHDCCYDHLKTQCGGIYKDYRYNFSQGNHCHSDKGSWCEQQLC 109
Db 61 DWCCQTHDCCYDHLKTQCGGIYKDN-----NKSIHCMD-----LSQRYC 100

Search completed: October 5, 2004, 19:41:12
Job time : 34.8667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 19:21:45 ; Search time 9.86 seconds
(without alignments)
1414.561 Million cell updates/sec

Title: US-09-830-321A-1

Perfect score: 852

Sequence: 1 MELALLGLVVMAGVPIQG.....YQKRLRFVWRPHCRGQTGPGC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401.5	47.1	146	A35493	phospholipase A2 (
2	399.5	46.9	146	A33394	phospholipase A2 (
3	395.5	46.4	144	PSHUYF	phospholipase A2 (
4	389.5	45.7	146	JU0283	phospholipase A2 (
5	389	45.7	145	I48093	phospholipase A2 (
6	365.5	42.9	146	I48342	phospholipase A2 (
7	347	40.7	138	A49959	phospholipase A2 (
8	335.5	39.4	138	PSRSBT	phospholipase A2 (
9	335.5	39.4	138	I51381	phospholipase A2 (
10	332	39.0	125	JX0052	phospholipase A2 (
11	331.5	38.9	138	PSRSB2	phospholipase A2 (
12	328.5	38.6	138	JC1342	phospholipase A2 (
13	320.5	37.6	122	S13900	phospholipase A2 (
14	319.5	37.5	137	S68429	myotoxin precursor
15	316.5	37.1	122	PSVIXF	phospholipase A2 (
16	314.5	36.9	138	S10992	ammodytin L precur
17	313.5	36.8	138	E48188	phospholipase A2 (
18	312.5	36.7	121	PC4024	phospholipase A2 h
19	312.5	36.7	122	PSABA	phospholipase A2 (
20	311.5	36.6	122	JX0063	phospholipase A2 (
21	311.5	36.6	138	D48188	phospholipase A2 (
22	310	36.4	138	S59522	phospholipase A2 (
23	309.5	36.3	138	S59522	phospholipase A2 (
24	307.5	36.1	121	PSSNAM	phospholipase A2 h
25	305.5	35.9	138	PSVIAC	phospholipase A2 (
26	305.5	35.9	138	S10333	ammodytoxin B prec
27	305.5	35.9	138	I51386	phospholipase A2 (
28	304.5	35.7	138	PSVIAA	phospholipase A2 (
29	302	35.4	138	I50098	phospholipase a2 -

ALIGNMENTS

RESULT 1

A35493

phospholipase A2 (EC 3.1.1.4) II precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 14-Sep-1990 #sequence revision 18-Nov-1992 #text_change 18-Jun-1999

C:Accession: A35493; S11388; S71310

R:Komada, M.; Kudo, I.; Inoue, K.

Biochem. Biophys. Res. Commun. 168, 1059-1065, 1990

A:Title: Structure of gene coding for rat group II phospholipase A-2.

A:Reference number: A35493; MUID:90267443; PMID:2346480

A:Accession: A35493

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-146 <KOM>

A:Cross-references: GB:M37127; NID:G204318; PIDN:AAA4123.1; PID:G204319

A:Note: The authors translated the codon TAT for residue 42 as Thr

R:Kusunoki, C.; Satoh, S.; Kobayashi, M.; Niwa, M.

Biochim. Biophys. Acta 1087, 95-97, 1990

A:Title: Structure of genomic DNA for rat platelet phospholipase A(2).

A:Reference number: S11388; MUID:90381322; PMID:2400792

A:Accession: S11388

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-146 <KUS>

A:Cross-references: EMBL:X51529; NID:G56930; PIDN:CAA35909.1; PID:G56931

R:Aarsman, A.J.; Schalkwijk, C.G.; Neys, F.W.; Iijima, N.; Wherrett, J.R.; van den Bosch,

Arch. Biochem. Biophys. 331, 95-103, 1996

A:Title: Purification and characterization of Ca(2+)-dependent phospholipases A(2) from r

A:Reference number: S71310; MUID:96268465; PMID:8660688

A:Accession: S71310

A:Molecule type: protein

A:Residues: 22-29, 'X', '31-32, 'X', '34 <AAR>

A:Experimental source: kidney

C:Superfamily: phospholipase A2

C:Keywords: carboxylic ester hydrolase; lipid degradation

F:68,113/Active site: His, Asp #status predicted

Query Match

Best Local Similarity 47.1%; Score 401.5; DB 2; Length 146;

Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

QY	1	MELALLGLVVMAGVPIQG.....YQKRLRFVWRPHCRGQTGPGC 59
DB	1	MKVLLLLAVVIMAFSGIQVQSLLFFGQMILPKTKRADVSFYGYCHGCGVGRGSPKDA 60
QY	60	TDWCCTQDCCYDHLKTKTCGCTYKDYRYNFQSGNIHCSDKGSCWCEQQLCACDKEVAFCL 119
DB	61	TDWCCTHDDCCYNLEKRCGCTKFLTYKFSYGGQISCSNTQDSCKQLCCQDKAAAEFC 120
QY	120	KNNLDITYQKRLRFYWRPHCRGQTGPGC 145
DB	121	ARNKXSYSLKQFYLNKFKCKGKTPSC 146

A:Gene: GDB:PLA2G2A; PLA2B; PLA2L
A:Cross-references: GDB:120296; OMIM:172411
A:Map position: 1p36.1-1p35
A:Introns: 14/1; 62/2; 98/1
C:Function:

A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
A:Note: the reaction is strongly enhanced when the phospholipid is condensed into a micelle
C:Superfamily: phospholipase A2
A:Keywords: calcium; carboxylic ester hydrolase; extracellular protein; lipid degradation
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-144/Product: phospholipase A2 IIA #status experimental <MAT>
F:46-137,48-64,63-117,69-144,70-110,79-103,97-108/Disulfide bonds: #status experimental
F:47,49,51,68/Binding site: calcium (His, Gly, Asp) #status predicted
F:67,111/Active site: His, Asp #status predicted

Query Match 46.4%; Score 395.5; DB 1; Length 144;
Best Local Similarity 47.6%; Pred. No. 3.9e-29;
Matches 69; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

QY 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGGLGGRGPKDAT 60
DB 1 MKTLLAVIMIFGLLQAHGNLVNFRMLKLTITGEALSYGFYCHGCGVGRGSPKDAT 60
QY 61 DWCCQTHDCCYDHLTKQCGIYKDYRYNFSQGNHCSDKSWCEQQIACDKEVAFCLK 120
DB 61 DRCCVTHDCCYKRLKRGCGTKFLSYKFSNGSRITCAKQDS-CRSQLCECDKAAATCFA 119
QY 121 RNLDTYQKRLRFYWRPHCRGQTGCG 145
DB 120 RNKTTYNKYQYYSNKHCRGKTPRC 144

RESULT 4

I48093
phospholipase A2 (EC 3.1.1.4) precursor (version 2) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 24-Jul-1997
C:Accession: J00283
R:Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.
J. Biochem. 106, 545-547, 1989
A:Title: Structure of cDNA coding for rat platelet phospholipase A2.
A:Reference number: J00131; MUID:90110043; PMID:2606907
A:Accession: J00283
A:Molecule type: mRNA
A:Residues: 1-146 <KOW>
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-146/Product: phospholipase A2 #status predicted <MAT>
F:68,113/Active site: His, Asp #status predicted

Query Match 45.7%; Score 389.5; DB 2; Length 146;
Best Local Similarity 47.3%; Pred. No. 1.4e-28;
Matches 69; Conservative 23; Mismatches 53; Indels 1; Gaps 1;

QY 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGGLGGRGPKDA 59
DB 1 MKVLLLLAVINAFSGIQVGSLLBFGQMLFKTKRADVSYGFYCHGCGVGRGSPKDA 60
QY 60 TDWCQTHDCCYDHLTKQCGIYKDYRYNFSQGNHCSDKSWCEQQIACDKEVAFCL 119
DB 61 TDWCCTHGCCYNLLEKRGCGTKFLTYKFSYRGQIISCSNDSCRKQLCCQDKAAAEFC 120
QY 120 KENLDYQKRLRFYWRPHCRGQTGCG 145
DB 121 ARNKXSYSLKYQFYPNKFCCKGKTPSC 146

RESULT 5

I48093
phospholipase A2 (EC 3.1.1.4) type II - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 18-Jun-1999

C:Accession: I48093
R:Vial, D.; Senoralle-Pose, M.; Havet, N.; Molio, L.; Vargaftig, B.B.; Touqui, L.
J. Biol. Chem. 270, 17327-17332, 1995
A:Title: Expression of the type-II phospholipase A2 in alveolar macrophages. Down-regulat
A:Reference number: I48093; MUID:95340522; PMID:7615534
A:Accession: I48093
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-145 <RES>
A:Cross-references: EMBL:X82631; NID:951010; PIDN:CAAS7953.1; PID:g951011
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:67,112/Active site: His, Asp #status predicted

Query Match 45.7%; Score 389; DB 2; Length 145;
Best Local Similarity 49.3%; Pred. No. 1.5e-28;
Matches 72; Conservative 20; Mismatches 52; Indels 2; Gaps 2;

QY 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGGLGGRGPKDA 59
DB 1 MKTLLLL-LVMASDLPQAHGHLKQFTEMIKLTITGKNGLTSGAYGCHGCGVGRGPKDA 59
QY 60 TDWCQTHDCCYDHLTKQCGIYKDYRYNFSQGNHCSDKSWCEQQIACDKEVAFCL 119
DB 60 TDRCCVRHDCYDRLMKRGCGTKFLNRYFTHKGSITCSVKQNSCQKQLCECDKAAAYCF 119
QY 120 KENLDYQKRLRFYWRPHCRGQTGCG 145
DB 120 AANLKSYRSRYQFYNGLCRGTPTSC 145

RESULT 6

I48342
phospholipase A2 (EC 3.1.1.4), secretory group II - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I48342; PC2009; S35948; I49352
R:Mulherkar, R.; Rao, R.S.; Wagie, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 195, 1254-1263, 1993
A:Title: Enhancing factor, a Paneth cell specific protein from mouse small intestines: pr
A:Reference number: I48342; MUID:94029955; PMID:8267767
A:Accession: I48342
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-146 <MULL>
A:Cross-references: EMBL:X74266; NID:g557247; PIDN:CAAS2325.1; PID:g557248
R:Mulherkar, R.; Rao, R.S.; Wagie, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 197, 351-352, 1993
A:Title: Enhancing factor, a paneth cell specific protein from mouse small intestines: pr
A:Reference number: PC2009; MUID:94071967; PMID:8250944
A:Accession: PC2009
A:Molecule type: mRNA
A:Residues: 22-146 <MUL2>
A:Note: correction of S35948
R:Mulherkar, R.; Rao, R.; Wagie, A.; Patki, V.; Deo, M.
submitted to the EMBL Data Library, July 1993
A:Reference number: S35948
A:Accession: S35948
A:Molecule type: mRNA
A:Residues: 22-115, 'R', 118-146 <MUL3>
A:Cross-references: EMBL:X74266
R:Kennedy, B.P.; Pavette, P.; Mudgett, J.; Vadas, P.; Pruzanski, W.; Kwan, M.; Tang, C.;
J. Biol. Chem. 270, 22378-22385, 1995
A:Title: A natural disruption of the secretory group II phospholipase A2 gene in inbred n
A:Reference number: I49352; MUID:95403435; PMID:7673223
A:Accession: I49352
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18, 'V', 20-85, 'K', 87-146 <KEN>
A:Cross-references: EMBL:U32358; NID:g984836; PIDN:AACS2252.1; PID:g984837
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:68,113/Active site: His, Asp #status predicted

A:Accession: S45647
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 17-138 <FAU>
A:Cross-references: EMBL:X16100
A:Accession: S46598
A:Molecule type: protein
A:Residues: 17-51 <FA2>
C:Comment: Crotoxin is a beta-neurotoxin.
C:Complex: heterodimer of acidic and basic chains
C:Function:
A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
A:Note: the reaction is strongly enhanced when the phospholipid is condensed into a micelle
C:Superfamily: phospholipase A2
C:Keywords: calcium; carboxylic ester hydrolase; heterodimer; lipid degradation; metallo
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-138/Product: crotoxin basic chain 2 #status experimental <MAT>
F:20,80/Binding site: micellar substrate (Gln, Tyr) #status predicted
F:42-131,44-60,59-111,65-138,66-104,73-97,91-102/Disulfide bonds: #status predicted
F:43,45,47,64/Binding site: calcium (Tyr, Gly, Asp) #status predicted
F:63,105/Active site: His, Asp #status predicted

Query Match 38.9%; Score 331.5; DB 1; Length 138;
Best Local Similarity 44.1%; Pred. No. 2.7e-23;
Matches 60; Conservative 21; Mismatches 52; Indels 3; Gaps 2;

QY 10 VMAGVPIQGGILNKNMKVQVTGKMPILSYWPGCHGCGGRQPKDATDWCCQTHDC 69
DB 6 IVAVLLGVESLLQFKNMKIKETRNAPFFAFYGCYCGWGGRPKDATDRCCFVHDC 65

QY 70 CYDHLKTQGGIYKDYRYNFSQNIHCSDKGWCQEQLCACDKEVAFCLRNLDITYOKR 129
DB 66 CYG--KLAKCNPKDIYRSLKSGYITCG-KGTWCKEIQICECDRAAECLRSLSITYKNE 122

QY 130 LRFYWRPHCRGQTGPGC 145
DB 123 YMFYDPSRCREPSETC 138

RESULT 12
JCL1342
Phospholipase A2 (EC 3.1.1.4) precursor - halys viper
C:Species: Agkistrodon halys (halys viper)
C:Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 13-Nov-1998
C:Accession: JCL1342
R:Pan, H.; Ou-Yang, L.L.; Yang, G.Z.; Zhou, Y.C.; Wu, X.F.
Acta Biochim. Biophys. Sin. 28, 579-582, 1996
A:Title: Cloning of the BPLA2 gene from Agkistrodon halys Pallas.
A:Reference number: JCL1342
A:Contents: Snake venom
A:Accession: JCL1342
A:Molecule type: mRNA
A:Residues: 1-138 <PAN>
C:Comment: This protein catalyzes the codon GAC for residue 54 as Asn
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-138/Product: phospholipase A2 #status predicted <MAT>

Query Match 38.6%; Score 328.5; DB 2; Length 138;
Best Local Similarity 43.4%; Pred. No. 5e-23;
Matches 59; Conservative 24; Mismatches 50; Indels 3; Gaps 2;

QY 10 VMAGVPIQGGILNKNMKVQVTGKMPILSYWPGCHGCGGRQPKDATDWCCQTHDC 69
DB 6 IVAVLLGVESLLQFKNMKIKETRNAPFFAFYGCYCGWGGRPKDATDRCCFVHDC 65

QY 70 CYDHLKTQGGIYKDYRYNFSQNIHCSDKGWCQEQLCACDKEVAFCLRNLDITYOKR 129
DB 66 CYE--KUTGCDPKWDITYSKNGTIVCGDDP--CKKEVCECDKAAALCFRNLITYOKR 122

QY 130 LRFYWRPHCRGQTGPGC 145

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OM protein - protein search, using sw model

Run on: October 5, 2004, 19:13:29 ; Search time 5.8 Seconds
(without alignments)
1301.754 Million cell updates/sec

Title: US-09-830-321A-1

Perfect score: 852

Sequence: 1 MELALLGLVVMAGVIPIQG.....YQKRLRFYWRPHCRGQTGDC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	846	99.3	145	1 PA2D_HUMAN	Q9unk4 homo sapien
2	624.5	73.3	144	1 PA2D_MOUSE	Q9wvf6 mus musculus
3	399.5	46.9	144	1 PA2A_RAT	P14423 rattus norv
4	395.5	46.4	144	1 PA2A_HUMAN	P14555 homo sapien
5	389	45.7	145	1 PA2M_CAVPO	P47711 cavia porce
6	371.5	43.6	146	1 PA2A_MOUSE	P31482 mus musculus
7	352	41.3	168	1 PA2F_HUMAN	Q9bzm2 homo sapien
8	347	40.7	138	1 PA2S_HUMAN	P39877 homo sapien
9	340.5	40.0	138	1 PA23_BOTAS	Q9pve3 bothrops as
10	336	39.4	122	1 PA22_BOTMO	Q91834 bothrops mo
11	336	39.4	168	1 PA2F_MOUSE	Q9gzt4 mus musculus
12	335.5	39.4	138	1 PA2B_CRODU	P07517 crotalus du
13	332	39.0	138	1 PA2W_TRIFL	Q02517 trimeresuru
14	331.5	38.9	138	1 PA2C_CRODU	P24027 crotalus du
15	330.5	38.8	138	1 PA2H_AGKAC	O57385 agkistrodon
16	330	38.7	137	1 PA2S_MOUSE	P97391 mus musculus
17	330	38.7	138	1 PA2Y_TRIFL	Q90y77 trimeresuru
18	329	38.6	138	1 PA2Q_TRIFL	Q81ig0 trimeresuru
19	328.5	38.6	121	1 PA22_BOTAS	P24605 bothrops as
20	328.5	38.6	138	1 PA24_AGRHP	O42187 agkistrodon
21	328.5	38.6	142	1 PA2A_AGRHP	Q91at9 bothrops ne
22	320.5	37.6	119	1 PA2M_BOTNE	P49121 agkistrodon
23	319.5	37.5	137	1 PA2H_AGKCL	P59264 trimeresuru
24	318.5	37.4	121	1 PA22_BOTPI	Q90z29 echis color
25	317.5	37.3	122	1 PA2A_TRIFL	P06860 trimeresuru
26	317.5	37.3	122	1 PA2B_TRIFL	P51433 rattus norv
27	317.5	37.3	138	1 PA21_ECHCO	P17935 vipera ammo
28	316.5	37.1	122	1 PA2C_TRIFL	Q90249 bothrops ja
29	315.5	37.0	137	1 PA25_RAT	P04417 agkistrodon
30	314.5	36.9	121	1 PA21_BOTPI	
31	313.5	36.8	138	1 PA2L_VIPAA	
32	312.5	36.7	121	1 PA2L_BOTUR	
33	312.5	36.7	122	1 PA21_AGKHA	

RESULT 1
PA2D_HUMAN
ID PA2D_HUMAN STANDARD; PRT; 145 AA.
AC Q9UNK4; Q9UK01;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase GIID) (GIID sPLA2) (PLA2IID)
DE (sPLA2)-IID) (Secretory-type PLA, stroma-associated homolog).
GN PLA2G2D OR SPLASH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., VARIANT GLY-80, AND CHARACTERIZATION.
RX MEDLINE=99386983; PubMed=10455175;
RA Ishizaki J., Suzuki N., Higashino K.-I., Yokota Y., Ono T.,
RA Kawamoto K., Fujii N., Arita H., Hanasaki K.;
RT "Cloning and characterization of novel mouse and human secretory
phospholipase A2s";
RL J. Biol. Chem. 274:24973-24979 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21040292; PubMed=11196711;
RA Shakhov A.N., Rubtsov A.V., Lyakhov I.G., Tumanov A.V.,
RA Nedospasov S.A.;
RT "SPLASH (PLA2) IID), a novel member of phospholipase A2 family, is
associated with lymphotoxin-deficiency";
RL Genes Immun. 1:191-199 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Wallis J.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
TX TISSUE=Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

ALIGNMENTS

34 311.5 36.6 122 1 PA23_AGKHP P14421 agkistrodon
35 311.5 36.6 138 1 PA2F_AGKRH Q9pvf3 agkistrodon
36 311.5 36.6 138 1 PA2P_TRIFL P20381 trimeresuru
37 310 36.4 138 1 PA2P_TRIFL Q92147 trimeresuru
38 309.5 36.3 138 1 PA2A_TRIMU Q90w39 trimeresuru
39 308.5 36.2 122 1 PA29_AGKHP Q42188 agkistrodon
40 308.5 36.2 142 1 PA2E_HUMAN Q9nzk7 homo sapien
41 308 36.2 138 1 PA2E_TRIFE Q8jly9 trimeresuru
42 307.5 36.1 121 1 PA28_DABRR P59071 daboia ruse
43 307.5 36.1 121 1 PA2H_AGKPI P04361 agkistrodon
44 307.5 36.1 137 1 PA2H_CERGO Q8uvu7 cerrophidic
45 306.5 36.0 137 1 PA2H_CROAT Q8uvz7 crotalus at

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. L-alpha-1-palmitoyl-2-linoleoyl phosphatidylethanolamine is more efficiently hydrolyzed than the other phospholipids examined.

CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.

CC -1- COFACTOR: Binds 1 calcium ion per subunit.

CC -1- SUBCELLULAR LOCATION: Secreted (Potential).

CC -1- TISSUE SPECIFICITY: Broadly expressed.

CC -1- MISCELLANEOUS: Maximally active at neutral to alkaline pH and with 2 mM Ca(2+).

CC -1- SIMILARITY: Belongs to the phospholipase A2 family.

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CC -----

DR EMBL; AF112982; AAD51390.1; -

DR EMBL; AF188625; AAF09020.1; -

DR EMBL; AL158172; CAC13159.1; -

DR EMBL; BC025706; AAH25706.1; -

DR HSSP; P14555; IPOD.

DR Genew; HGNC:9033; PLA2G2D.

DR MIM; 605630; -

DR GO; GO:0005576; C:extracellular; TAS.

DR GO; GO:0004624; P:secreted phospholipase A2 activity; TAS.

DR GO; GO:0006954; P:inflammatory response; TAS.

DR GO; GO:0006644; P:phospholipid metabolism; TAS.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; phoslip; 1.

DR PRINTS; PR00389; PHPLIPASEA2.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1.

DR PROSITE; PS00119; PA2_ASP; 1.

DR PROSITE; PS00118; PA2_HIS; 1.

KW Hydrolase; Lipid degradation; Signal; Calcium; Polymorphism.

FT SIGNAL 1 20

FT CHAIN 21 145

FT ACT_SITE 67 112

FT ACT_SITE 112 112

FT DISULFID 46 138

FT DISULFID 48 64

FT DISULFID 63 118

FT DISULFID 69 145

FT DISULFID 70 111

FT DISULFID 79 104

FT DISULFID 97 109

FT CARBOHYD 89 89

FT METAL 47 47

FT METAL 49 49

FT METAL 51 51

FT METAL 68 68

FT VARIANT 80 80

FT SEQUENCE 145 AA; 16546 MW; CF3A49DE516BD1EF CRC64; /FTId=VAR_012741.

Query Match 99.3%; Score 846; DB 1; Length 145;

Best Local Similarity 99.3%; Pred. No. 1.7e-78;

Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MELALLCGLVVWAGVIPIQGGILNLNWKVQVTKGWPILSYWPGYCHGGLGGRGQPKDAT 60

DB 1 MELALLCGLVVWAGVIPIQGGILNLNWKVQVTKGWPILSYWPGYCHGGLGGRGQPKDAI 60

OY 61 DWCCQTHDCCYDLHKTGCGGIYKDYRYNPSQGNHCSKGSWCEQQLCACDKEVAFCLK 120

DB 61 DWCCQTHDCCYDLHKTGCGGIYKDYRYNPSQGNHCSKGSWCEQQLCACDKEVAFCLK 120

OY 121 RNLDTYQKRLRFYWRPHCRGQTGQC 145

DB 121 RNLDTYQKRLRFYWRPHCRGQTGQC 145

RESULT 2

PA2D MOUSE

ID PA2D MOUSE STANDARD; PRT; 144 AA.

AC Q9WVF6; Q9JLK0;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Group IID secretory phospholipase A2 precursor (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase GIIID) (GIIID sPLA2) (sPLA2)-IID) (Secretory-type PLA, stroma-associated homolog).

DE PLA2G2D OR PLA2A2 OR SPLASH.

GN Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

OX [1]

RN SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.

RP STRAIN=BALB/c;

RC MEDLINE=99386983; PubMed=10455175;

RX Ishizaki J., Suzuki N., Higashino K.-I., Yokota Y., Ono T., Kawamoto K., Fujii N., Arita H., Hanasaki K.;

RA "Cloning and characterization of novel mouse and human secretory phospholipase A2s."

RL J. Biol. Chem. 274:24973-24979(1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=99315857; PubMed=10383420;

RA Valentin E., Koduri R.S., Scimeca J.-C., Carle G., Gelb M.H., Lazdunski M., Lambeau G.;

RA "Cloning and recombinant expression of a novel mouse-secreted phospholipase A2."

RL J. Biol. Chem. 274:19152-19160(1999).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RX MEDLINE=C57BL/6 X 129;

RC MEDLINE=21040292; PubMed=11196711;

RA Shakhov A.N., Rubtsov A.V., Lyakhov I.G., Tumanov A.V., Nedospasov S.A.;

RA "SPLASH (PLA2)IID), a novel member of phospholipase A2 family, is associated with lymphotoxin-deficiency."

RL Genes Immun. 1:191-199(2000).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S., Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.;"

RL Nature 409:685-690(2001).

CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-

CC acyl groups in 3-sn-phosphoglycerides. L-alpha-1-palmitoyl-2-

CC linoleoyl phosphatidylethanolamine is more efficiently hydrolyzed

CC than the other phospholipids examined.

CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-

CC acylglycerophosphocholine + a fatty acid anion.

CC -!- COFACTOR: Binds 1 calcium ion per subunit.

CC -!- SUBCELLULAR LOCATION: Secreted (isoform 1) and Cytoplasmic

CC (isoform 2) (Potential).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q9WVF6-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q9WVF6-2; Sequence=VSP 004508;

CC -!- TISSUE SPECIFICITY: Expressed in several tissues including

CC pancreas, spleen, thymus, skin, lung, and ovary.

CC -!- SIMILARITY: Belongs to the phospholipase A2 family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF112983; AAD51391.1; -;

DR EMBL; AF124374; AAD42773.1; -;

DR EMBL; AF188624; AAF09019.1; -;

DR EMBL; AF169407; AAF42987.1; -;

DR EMBL; AF169408; AAF42988.1; -;

DR EMBL; AK018005; BAB31033.1; -;

DR EMBL; AK004232; -; NOT_ANNOTATED_CDS.

DR HSSP; P24605; 1CLP.

DR MGB; MGI:1341796; Pla2g2d.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; phoslip; 1.

DR PRINTS; PR00389; PPHPLIPASEA2.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2C; 1.

DR PROSITE; PS00119; PA2_ASP; 1.

DR PROSITE; PS00118; PA2_HIS; 1.

DR KW Hydrolase; Lipid degradation; Signal; Calcium; Alternative splicing.

FT SIGNAL 1 19

FT CHAIN 20 144

FT ACT_SITE 66 66

FT ACT_SITE 111 111

FT DISULFID 45 137

FT DISULFID 47 63

FT DISULFID 62 117

FT DISULFID 68 144

FT DISULFID 69 110

FT DISULFID 78 103

FT DISULFID 96 108

FT CARBOHYD 99 99

FT METAL 46 46

FT METAL 48 48

FT METAL 50 50

FT METAL 67 67

FT VARSPLIC 1 26

FT SEQUENCE 144 AA; 16164 MW; 7697ADA07F8D270A CRC64;

Query Match 73.3%; Score 624.5; DB 1; Length 144;

Best Local Similarity 71.0%; Pred. No. 3.8e-56;

Matches 103; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

QY 1 MELALLCGLVVMAGVPIQGGILNLNKVKQVTKMPILSYWPGYCHGGLGGGQPKDAT 60

Db 1 MELALLCGL-LIAGTATQGGILNLNKVTHMTGKKAFFSYWPGYCHGGLGGGQPKDAT 59

QY 61 DMCCQTHDCCYDHLTKTQGGIYKDYRYNFSOGNIHCSKSWCEQOLCACDKEVAFCLK 120

Db 60 DMCCQKHDCCYAHLKIDGCKSLTDNYKYSISQGTICSDNGSWCEQOLCACDKEVAFCLK 119

QY 121 RNLDYQKRLRYWRPHCRGQTPGC 145

Db 120 QNLDSYNKRLYYWRPRCKGKTPAC 144

RESULT 3

PA2A_RAT STANDARD; PRT; 146 AA.

AC PL4423;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)

DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)

DE (GIIC sPLA2).

GN PLA2G2A.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=Sprague-Dawley; TISSUE=platelet;

RC MEDLINE=90110043; PubMed=2606907;

RA Komada M., Kudo I., Mizushima H., Kitamura N., Inoue K.;

RT "Structure of cDNA coding for rat platelet phospholipase A2.;"

RL J. Biochem. 106:545-547(1989).

RN [2]

RP SEQUENCE FROM N.A.

RX TISSUE=Spleen;

RC MEDLINE=90267443; PubMed=2346480;

RA Komada M., Kudo I., Inoue K.;

RT "Structure of gene coding for rat group II phospholipase A2.;"

RL Biochem. Biophys. Res. Commun. 168:1059-1065(1990).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=89350908; PubMed=2764915;

RA Ishizaki J., Ohara O., Nakamura E., Tamaki M., Ono T., Kanda A.,

RT "cDNA cloning and sequence determination of rat membrane-associated

RT phospholipase A2.;"

RL Biochem. Biophys. Res. Commun. 162:1030-1036(1989).

RN [4]

RP SEQUENCE FROM N.A.

RX STRAIN=Sprague-Dawley; TISSUE=Liver;

RC MEDLINE=90381322; PubMed=2400792;

RA Kusunoki C., Satoh S., Kobayashi M., Niwa M.;

RT "Structure of genomic DNA for rat platelet phospholipase A2.;"

RL Biochim. Biophys. Acta 1087:95-97(1990).

RN [5]

RP SEQUENCE OF 22-146.

RX STRAIN=Wistar; TISSUE=platelet;

RC MEDLINE=89174508; PubMed=3235451;

RA Hayakawa M., Kudo I., Tomita M., Nojima S., Inoue K.;

RT "The primary structure of rat platelet phospholipase A2.;"

RL J. Biochem. 104:767-772(1988).

RN [6]

RP SEQUENCE OF 22-57.

RX TISSUE=Spleen;

RC MEDLINE=88186890; PubMed=3356705;

RA Ono T., Tojo H., Kuramitsu S., Kagamiyama H., Okamoto M.;

RT "Purification and characterization of a membrane-associated

RT phospholipase A2 from rat spleen. Its comparison with a cytosolic

RT phospholipase A2 S-1.;"

RL J. Biol. Chem. 263:5732-5738(1988).

[7]
RN SEQUENCE OF 22-46.
RP TISSUE=Platelet;
RX MEDLINE=89007474; PubMed=3654593;
RA Hayakawa M., Horigome K., Kudo I., Tomita M., Notima S., Inoue K.;
RT "Amino acid composition and NH2-terminal amino acid sequence of rat platelet secretory phospholipase A2.";
RL J. Biochem. 101:1311-1314(1987).
[8]
RN SEQUENCE OF 22-45.
RP TISSUE=Liver;
RX MEDLINE=89255484; PubMed=2722857;
RA Aarsman A. J., de Jong J.G.N., Arnoldussen E., Neys F.W.,
van Wassenaar P.D., van den Bosch H.;
RT "Immunofluorescent purification, partial sequence, and subcellular localization of rat liver phospholipase A2.";
RL J. Biol. Chem. 264:10008-10014(1989).
CC -!- FUNCTION: Thought to participate in the regulation of the phospholipid metabolism in biomembranes including eicosanoid biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- MISCELLANEOUS: Group II phospholipase A2 is found in many cells and is also extracellularly. The membrane-bound and secreted forms are identical and are encoded by a single gene.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC
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CC
CC EMBL; D00523; BAA00410.1; -
CC EMBL; M37127; AAA41223.1; -
CC EMBL; M25148; AAA41920.1; -
CC EMBL; X51529; CAA35909.1; -
CC PIR; A33394; A33394.
CC HSP; P44555; LP0D.
CC InterPro; IPR001211; PhospholipaseA2.
CC Pfam; PF00068; phoslip; 1.
CC PRINTS; PR00389; PHPLIPASEA2.
CC ProDom; PD00303; PhospholipaseA2; 1.
CC SMART; SM00085; PA2c; 1.
CC PROSITE; PS00118; PA2_HIS; 1.
CC PROSITE; PS00119; PA2_ASP; 1.
CC Hydrolase; Lipid degradation; Membrane; Signal; Calcium.
KW SIGNAL
FT 1 21
FT CHAIN 22 146
FT ACT_SITE 68 68
FT ACT_SITE 113 113
FT DISULFID 47 139
FT DISULFID 49 65
FT DISULFID 64 119
FT DISULFID 70 146
FT DISULFID 71 112
FT DISULFID 80 105
FT DISULFID 98 110
FT METAL 48 48
FT METAL 50 50
FT METAL 52 52
FT METAL 69 69
FT METAL 135 135
FT VARIANT 22 22
FT CONFLICT 63 63

FT CONFLICT 69 69 D -> E (IN REF. 5).
FT CONFLICT 78 78 R -> S (IN REF. 5).
FT CONFLICT 85 85 L -> V (IN REF. 3).
FT CONFLICT 121 121 A -> S (IN REF. 5).
SQ SEQUENCE 146 AA; 16294 MW; 60DDC9E79BF109F7 CRC64;
Query Match 46.9%; Score 399.5; DB 1; Length 146;
Best Local Similarity 47.9%; Pred. No. 2e-33;
Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;
QY 1 METALLGLVMA-GVTPIQGILNLMKWKQVTKGMPILSYWPFYCHGCGGRGQPKDA 59
DB 1 MKVLLLVAVIMAFSGIQVGSLLFCQMILFKTKGADVSYGFGCHGCGGRGSPKDA 60
QY 60 TDMCCQTHDCCYDHLTKTQGGCIYKDYRYNFSQNIHCSKDGSCWCEQOLCACDEKVAFL 119
DB 61 TDMCCVTHDCYNNLEKRGCGTRFLTYKFSYRGQISCSNQNDSRQQLCQCDKAAAEFCF 120
QY 120 KRNLDTYQKRLRFYWRHCRGQTPGC 145
DB 121 ARNKKSYSLKYQFYFNPKFCRGTPTSC 146
RESULT 4
PA2A HUMAN STANDARD; PRT; 144 AA.
AC P14555; O9UCD2;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phospholipase A2, membrane associated precursor (RC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
DE (GIIC sPLA2) (Non-pancreatic secretory phospholipase A2) (NFS-PLA2).
GN PLA2G2A OR PLA2B OR RASFA-A OR PLA2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Rheumatoid arthritic synovial fluid;
RX MEDLINE=89174566; PubMed=2525608;
RA Seilhamer J.J., Fruzanski W., Vadas P., Plant S., Miller J.A.,
Kloss J., Johnson L.K.;
RT "Cloning and recombinant expression of phospholipase A2 present in rheumatoid arthritic synovial fluid.";
RL J. Biol. Chem. 264:5335-5338(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89174633; PubMed=2525633;
RA Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,
Tizard R., Pepinsky R.B.;
RT "Structure and properties of a human non-pancreatic phospholipase A2.";
RL J. Biol. Chem. 264:5768-5775(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91050834; PubMed=2239446;
RA Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;
RT "Structure and properties of a secreted phospholipase A2 from human platelets.";
RL Adv. Exp. Med. Biol. 275:35-53(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5].
 RP SEQUENCE OF 21-144.
 RC TISSUE=Spleen;
 RX MEDLINE=89374261; PubMed=2775276;
 RA Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;
 RT "The primary structure of a membrane-associated phospholipase A2 from
 RT human spleen.";
 RL Biochem. Biophys. Res. Commun. 163:42-48(1989).
 RN [6].
 RP SEQUENCE OF 21-54.
 RC TISSUE=Synovial fluid;
 RX MEDLINE=89197814; PubMed=3240982;
 RA Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;
 RT "Amino acid composition and NH2-terminal amino acid sequence of human
 RT phospholipase A2 purified from rheumatoid synovial fluid.";
 RL J. Biochem. 104:326-328(1988).
 RN [7].
 RP SEQUENCE OF 21-33.
 RC TISSUE=Spleen;
 RX MEDLINE=89076274; PubMed=3202859;
 RA Lai C.Y., Wada K.;
 RT "Phospholipase A2 from human synovial fluid: purification and
 RT structural homology to the placental enzyme.";
 RL Biochem. Biophys. Res. Commun. 157:488-493(1988).
 RN [8].
 RP SEQUENCE OF 21-75.
 RC TISSUE=ileal mucosa;
 RX MEDLINE=94002200; PubMed=8399335;
 RA Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.;
 RT "Purification and characterization of a phospholipase A2 from human
 RT ileal mucosa.";
 RL Biochim. Biophys. Acta 1170:125-130(1993).
 RN [9].
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=91287826; PubMed=2062381;
 RA Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
 RA Gamboa G., Goodson T. Jr., Hermann R.B., Kramer R.M., McClure D.B.,
 RA Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,
 RA Warrick M.W., Jones N.D.;
 RT "Structure of recombinant human rheumatoid arthritic synovial fluid
 RT phospholipase A2 at 2.2-A resolution.";
 RL Nature 352:79-82(1991).
 RN [10].
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=92054586; PubMed=1948070;
 RA Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,
 RA Sigler P.B.;
 RT "Structures of free and inhibited human secretory phospholipase A2
 RT from inflammatory exudate.";
 RL Science 254:1007-1010(1991).
 RN [11].
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=95393225; PubMed=7664108;
 RA Schevitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K.,
 RA Dillard R.D., Drahaim S.E., Hartley L.G., Jones N.D., Mihelich E.D.,
 RA Olkowski J.L., Snyder D.W., Dand S.C., Wery J.-P.;
 RT "Structure-based design of the first potent and selective inhibitor
 RT of human non-pancreatic secretory phospholipase A2.";
 RL Nat. Struct. Biol. 2:458-465(1995).
 RN [12].

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=98207049; PubMed=9538252;
 RA Kitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;
 RT "Crystal structure of human secretory phospholipase A2-IIA complex
 RT with the potent indolizine inhibitor 120-1032.";
 RL J. Biochem. 123:619-623(1998).
 CC -1- FUNCTION: Thought to participate in the regulation of the
 CC phospholipid metabolism in biomembranes including eicosanoid
 CC biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -1- COFACTOR: Binds 1 calcium ion per subunit.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.
 CC -1- MISCELLANEOUS: Group II phospholipase A2 is found in many cells
 CC and also extracellularly. The membrane-bound and secreted forms
 CC are identical and are encoded by a single gene.
 CC -1- SIMILARITY: Belongs to the phospholipase A2 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M22430; AAA36550.1; -;
 DR EMBL; M22431; AAA36549.1; -;
 DR EMBL; BC005919; AAH05919.1; -;
 DR PIR; A32862; PSUUVF
 DR PDB; 1AYP; 31-JUL-95.
 DR PDB; 1BEC; 31-OCT-93.
 DR PDB; 1POD; 31-OCT-93.
 DR PDB; 1POE; 31-OCT-93.
 DR PDB; 1KVO; 07-JUL-97.
 DR PDB; 1DB4; 12-NOV-99.
 DR PDB; 1DB5; 12-NOV-99.
 DR PDB; 1DCY; 12-NOV-99.
 DR Genew; HGNC:9031; PLA2G2A.
 DR MIM; 172411; -;
 DR GO; GO:0004623; F:phospholipase A2 activity; TAS.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR PRINIS; PR00389; PHPLIPASEA2.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR SMART; SM00085; PA2C; 1.
 DR PROSITE; PS00118; PA2_HIS; 1.
 DR PROSITE; PS00119; PA2_ASP; 1.
 KW Hydrolase; Lipid degradation; Membrane; Signal; Calcium;
 KW 3D-structure.
 FT SIGNAL 1 20
 FT CHAIN 21 144 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
 FT ACT_SITE 67 67 BY SIMILARITY.
 FT ACT_SITE 111 111 BY SIMILARITY.
 FT DISULFID 46 137
 FT DISULFID 48 64
 FT DISULFID 63 117
 FT DISULFID 69 144
 FT DISULFID 70 110
 FT DISULFID 79 103
 FT DISULFID 97 108
 FT METAL 47 47
 FT METAL 49 49
 FT METAL 51 51
 FT METAL 68 68
 FT HELIX 22 33
 FT HELIX 37 40
 FT TURN 41 41
 FT TURN 45 47
 FT HELIX 59 75
 FT TURN 76 78
 FT TURN 88 91
 FT STRAND 88 91

CALCIUM (VIA CARBONYL OXYGEN).
 CALCIUM (VIA CARBONYL OXYGEN).
 CALCIUM (VIA CARBONYL OXYGEN).
 CALCIUM.

RP SEQUENCE FROM N.A.
 RC STRAIN=C3H;
 RX MacPhee M., Chepenik K.P., Liddell R.A., Nelson K.K., Siracusa L.D.,
 RA Buchberg A.M.;
 RA "The secretory phospholipase A2 gene is a candidate for the Mom1
 RT locus, a major modifier of ApcMin-induced intestinal neoplasia";
 RL Cell 81:957-966(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=2388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 22-146 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Small intestine;
 RX MEDLINE=9402955; PubMed=8267767;
 RA Mulherkar R., Rao R.S., Wagie A.S., Patki V., Deo M.G.;
 RA "Enhancing factor, a Paneth cell specific protein from mouse small
 RT intestines: predicted amino acid sequence from RT-PCR amplified cDNA
 RT and its expression";
 RL Biochem. Biophys. Res. Commun. 195:1254-1263(1993).
 RN [6]
 RP ERATUM.
 RX MEDLINE=94071967; PubMed=8250944;
 RA Mulherkar R., Rao R.S., Wagie A.S., Patki V., Deo M.G.;
 RA Biochem. Biophys. Res. Commun. 197:351-352(1993).
 RN [7]
 RP PRELIMINARY SEQUENCE OF 22-41.
 RC TISSUE=Small intestine;
 RX MEDLINE=93146172; PubMed=8425615;
 RA Mulherkar R., Rao R., Rao L., Patki V., Chauhan V.S., Deo M.G.;
 RA "Enhancing factor protein from mouse small intestines belongs to the
 RT phospholipase A2 family";
 RL FEBS Lett. 317:263-266(1993).
 CC -1- FUNCTION: May play a role in cell proliferation, by increasing the
 CC binding of EGF to the cells and thereby modulating its action. In
 CC doing so, this isozyme binds to a membrane-associated receptor
 CC distinct from the EGF receptor and which could be a heparan-
 CC sulfate proteoglycan located on the cell membrane.
 CC -1- FUNCTION: P2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.
 CC -1- TISSUE SPECIFICITY: Mainly in the Paneth cells adjacent to the
 CC stem population in the small intestines. Also expressed in
 CC regenerating liver and hyperplastic esophageal epithelium.
 CC -1- POLYMORPHISM: In strains 129/Sv, B10.RIII and C57BL/6, a
 CC polymorphism causes a frameshift and premature truncation of the
 CC protein, rendering it inactive. Strains BALB/c, C3H/He, DBA/1,
 CC DBA/2, MRL and NZB/BN contain the normal protein while strain CD-
 CC 1 is heterozygous for the mutation.

CC -1- SIMILARITY: Belongs to the phospholipase A2 family.
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 CC -----
 CC EMBL; X74266; CAA52325.1; -;
 CC EMBL; U2358; AAC52252.1; -;
 CC EMBL; U2844; AAB06315.1; ALT INIT.
 CC EMBL; BC045156; AAH45156.1; -;
 CC PIR; I48342; I48342;
 CC PIR; S29495; S29495;
 CC HSP; P14555; IPOD.
 CC MGD; MGI:104642; P1a2g2a.
 CC InterPro; IPR001211; PhospholipaseA2.
 CC Pfam; PF00068; phoslip; 1
 CC PRINTS; PR00389; PHPLIPASEA2.
 CC ProDom; PDOM00303; PhospholipaseA2; 1.
 CC SMART; SMO0085; PA2C; 1.
 CC PROSITE; PS00118; PA2_HIS; 1.
 CC PROSITE; PS00119; PA2_ASP; 1.
 CC Hydrolase; Lipid degradation; Calcium; Growth regulation; Signal;
 CC Membrane; Polymorphism.
 CC SIGNAL 1 21
 CC CHAIN 22 146 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.
 CC ACT_SITE 68 68 BY SIMILARITY.
 CC ACT_SITE 113 113 BY SIMILARITY.
 CC DISULFID 47 133 BY SIMILARITY.
 CC DISULFID 49 65 BY SIMILARITY.
 CC DISULFID 64 119 BY SIMILARITY.
 CC DISULFID 70 146 BY SIMILARITY.
 CC DISULFID 71 112 BY SIMILARITY.
 CC DISULFID 80 105 BY SIMILARITY.
 CC DISULFID 98 110 BY SIMILARITY.
 CC METAL 48 48 CALCIUM (VIA CARBONYL OXYGEN)
 CC METAL 50 50 CALCIUM (VIA CARBONYL OXYGEN)
 CC METAL 52 52 CALCIUM (VIA CARBONYL OXYGEN)
 CC METAL 69 69 CALCIUM (BY SIMILARITY).
 CC CONFLICT 19 19 V -> D (IN REF. 1).
 CC CONFLICT 86 86 K -> T (IN REF. 1).
 CC SEQUENCE 146 AA; 16145 MW; AB904F6B3B1BA5C7 CRC64;
 CC -----
 CC Query Match 43.6%; Score 371.5; DB 1; Length 146;
 CC Best Local Similarity 47.3%; Pred. No. 1.3e-30;
 CC Matches 69; Conservative 19; Mismatches 57; Indels 1; Gaps 1;
 CC -----
 CC Qy 1 MELALLGLVMA-GVPIQGGIILNKMVKQTKMPILSYWPGYCHGLGGRGQPKDA 59
 CC Db 1 MKVLLLAASIMAFSGTQVGNATQFGEMRLTKGKAEISYAFYGCGLGGKGSPPDA 60
 CC Qy 60 TDMCCQTHDCYDHLTKTQGGYKDYRNFNSQNHCHSDKGSWCEQOLCACDKEVAFCL 119
 CC Db 61 TDRCCVTHDCYKSLKSGGTGKLLKYKHQSGQTCSANQNSQKRLCQCDKAAAEFCF 120
 CC Qy 120 KRNLDYQKELRFRWPHRCGTPGC 145
 CC Db 121 ARNKTYSLKYQFYPMNFCGKPKC 146
 CC -----
 CC RESULT 7
 CC PA2F HUMAN
 CC ID PA2F HUMAN STANDARD; PRT; 168 AA.
 CC AC Q9BZM2; Q9H506;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)


```

CC EMBL; U03090; AAC2886.1; -.
DR GO; GO:004625; F:calcium-dependent secreted phospholipase A2; TAS.
DR GO; GO:006644; P:phospholipid metabolism; TAS.
DR PIR; A49959; A49959.
DR HSP; P14421; 1A2A.
DR Genew; HGNC:9038; PLA2G5.
DR MIM; 601192; -.
DR GO; GO:000576; C:extracellular; TAS.
DR GO; GO:004625; F:calcium-dependent secreted phospholipase A2; TAS.
DR GO; GO:006644; P:phospholipid metabolism; TAS.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD00303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR KW Hydrolyase; Lipid degradation; Calcium; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138
FT ACT_SITE 67 67
FT ACT_SITE 111 111
FT DISULFID 46 137
FT DISULFID 48 64
FT DISULFID 63 117
FT DISULFID 70 110
FT DISULFID 79 103
FT DISULFID 97 108
FT METAL 47 47
FT METAL 49 49
FT METAL 51 51
FT METAL 68 68
FT SEQUENCE 138 AA; 15674 MW; 0D17DC76E55F42BC CRC64;
SQ
Query Match 40.7%; Score 347; DB 1; Length 138;
Best Local Similarity 43.6%; Pred. No. 3.7e-28;
Matches 58; Conservative 27; Mismatches 36; Indels 12; Gaps 2;
QY 12 MAGVIP-----LOGGIILNLMVKVQTKMPILSYWPGCHGLGRGQPKDAT 60
Db 1 MKGLPLANFLACVPAVQGLLDLKSIEKVTGNALTYGFYCYCGWGRGTPKDG 60
QY 61 DWCCQTHDCYDHLKTCGGYKDYRYNFSQGNHSCDKGSWCEQQLCACDKEVAFCLK 120
Db 61 DWCCWAHDHCYGRLEKGNIRTSQYKRFANGVVTCT-EPGPFCHVNLACDRKLIVYCLK 119
QY 121 RNLDYQKRLRFY 133
Db 120 RNLSRYNPQYQYF 132
RESULT 9
PA23_BOTAS STANDARD; PRT; 138 AA.
AC Q9PVE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2 homolog 3 precursor (Myotoxin III) (M1-3-3).
OS Bothrops asper (terciopelo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8722;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Pescatori M., Grasso A., Rufini S.;
RT "Molecular cloning of a K-42 PLA2-like myotoxin from the snake
RT Bothrops asper.";
```

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RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Myotoxic protein that lacks enzymatic activity (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- MISCELLANEOUS: Does not bind calcium as one of the calcium binding
CC ligands is lost (Asp->Lys in position 64) (Probable).
CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC subfamily.
CC
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CC
CC EMBL; AF109911; AAF14241.1; -.
DR HSP; P24605; 1CLP.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD00303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR KW Toxin; Signal; Multigene family.
FT SIGNAL 1 16
FT CHAIN 17 138
FT ACT_SITE 63 63
FT ACT_SITE 105 105
FT DISULFID 42 132
FT DISULFID 44 60
FT DISULFID 59 111
FT DISULFID 65 138
FT DISULFID 66 104
FT DISULFID 73 97
FT DISULFID 91 102
FT SEQUENCE 138 AA; 15559 MW; AF7491F7E3049BF2 CRC64;
SQ
Query Match 40.0%; Score 340.5; DB 1; Length 138;
Best Local Similarity 47.4%; Pred. No. 1.7e-27;
Matches 64; Conservative 21; Mismatches 43; Indels 7; Gaps 4;
QY 10 VWAGVPIQGGIILNLMVKVQTKMPILSYWPGCHGLGRGQPKDATWCQTHDC 69
Db 9 VLVGV---EGSLVELGKMLQETGKNPVTSYGAYGNCVGLGRGPKDATDRCCYVHKC 65
QY 70 CYDHLKTCGGYKDYRYNFSQGNHSCDKGSWCEQQLCACDKEVAFCLKRNLDYQKR 129
Db 66 CYK--KLTGCPKPKDYRSYKDKTIVCGNN--CLKELCECDKAVAICLRKLDYNNK 122
QY 130 LR-FYWRPHCRGQTP 143
Db 123 YKNNYLPKPFCKKADP 137
RESULT 10
PA22_BOTMO STANDARD; PRT; 122 AA.
AC Q9I834;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2 homolog 2 (Myotoxin II) (MjTX-II) (M-VI).
OS Bothrops moojeni (lance-headed viper) (Caissaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=98334;
RN [1]
RP SEQUENCE OF 1-52, AND CHARACTERIZATION.
RC TISSUE=Venom;
```

RX MEDLINE=98299483; PubMed=9637370;
 RA Soares A.M., Rodrigues V.M., Honsi-Brandeburgo M.I., Toyama M.H.,
 RA Lombardi F.R., Arni R.K., Giglio J.R.;
 RT "A rapid procedure for the isolation of the Lys-49 myotoxin II from
 RT Bothrops moojeni (caissaca) venom: biochemical characterization,
 RT crystallization, myotoxic and edematogenic activity.";
 RL Toxicon 36:503-514(1998).
 RN [2]
 RP SEQUENCE OF 15-122 FROM N.A.
 RC TISSUE=Venom gland;
 RA Soares A.M., Ward R.J., Rodrigues-Simioni L., Lomonte B.,
 RA Gutierrez J.M., Guerra-Sa R., Rodrigues V., Fontes M.R.M., Arni R.K.,
 RA Giglio J.R.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RC TISSUE=Venom;
 RA de Azevedo W.F., Ward R.J., Lombardi F.R., Giglio J.R., Soares A.M.,
 RA Fontes M.R.M., Arni R.K.;
 RT "Crystal structure of myotoxin-II: a myotoxic phospholipase A2
 RT homologue from Bothrops moojeni venom.";
 RL Protein Pept. Lett. 4:329-334(1997).
 CC -!- FUNCTION: Displays myotoxin and edema-inducing activities. Lacks
 CC PA2 enzymatic activity as well as of hemorrhagic, anticoagulant
 CC and coagulant activities.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: Does not bind calcium as one of the calcium binding
 CC ligands is lost (Asp->Iys in position 48).
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
 CC subfamily.
 CC
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 CC
 CC EMBL; AF145759; AAF66702.1; -.
 DR HSP; P82287; 1QLL.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR PRINTS; PR00389; PPHPLIPASEA2.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR SMART; SM00085; PA2C; 1.
 DR PROSITE; PS00119; PA2 ASP; 1.
 DR PROSITE; PS00118; PA2 HIS; 1.
 DR Toxin; Multigene family.
 KW ACT_SITE 47 47 BY SIMILARITY.
 FT ACT_SITE 89 89 BY SIMILARITY.
 FT DISULFID 26 116 BY SIMILARITY.
 FT DISULFID 28 44 BY SIMILARITY.
 FT DISULFID 43 95 BY SIMILARITY.
 FT DISULFID 49 122 BY SIMILARITY.
 FT DISULFID 50 88 BY SIMILARITY.
 FT DISULFID 57 81 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 FT CONFLICT 18 18 A -> V (IN REF. 2).
 SQ SEQUENCE 122 AA; 13887 MW; 120AA53FAB3309CB CRC64;
 Query Match 39.4%; Score 336; DB 1; Length 122;
 Best Local Similarity 50.4%; Pred. No. 4.1e-27;
 Matches 62; Conservative 15; Mismatches 42; Indels 4; Gaps 3;
 QY 22 ILNLMKRVQVTKGKPILSYWPYCHGCGRQPKDATTWCQTHDCYDHLKTKGCGI 81
 Db 2 LPELGMILQETGKPKAKSYGVYGCNCGVGRGKPKDATTDCYVHKCCYK--KLGCDF 59
 QY 82 YKDYRYNFSQGNHSCDGSWCCEQQLCACDEKVAFLKRLNLDYKRLRF-YWRPHCRG 140
 Db 60 KDRYSYSWKDKTGVGNNNS-CLKELCECDKAVAIKRLNLDYKRYNYLKPFCCK 118

QY 141 QTP 143
 Db 119 ADP 121
 RESULT 11
 PA2F MOUSE STANDARD; PRT; 168 AA.
 ID -PA2F MOUSE
 AC OSQZT4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Group IIF secretory phospholipase A2 precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase GIIF) (GIIF SPLA2) (SPLA(2)-IIF).
 GN PLA2G2F.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20002639; PubMed=10531313;
 RA Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.;
 RT "On the diversity of secreted phospholipases A2. Cloning, tissue
 RT distribution, and functional expression of two novel mouse group II
 RT enzymes.";
 RL J. Biol. Chem. 274:31195-31202(1999).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides. Hydrolyzes
 CC phosphatidylglycerol versus phosphatidylcholine with a 15-fold
 CC preference (by similarity).
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
 CC
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 CC
 CC EMBL; AF166099; AAF04500.2; -.
 DR HSP; P00593; 4BP2.
 DR MGD; MGI:1349661; Pla2g2f.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR PRINTS; PR00389; PPHPLIPASEA2.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR SMART; SM00085; PA2C; 1.
 DR PROSITE; PS00119; PA2 ASP; FALSE_NEG.
 DR PROSITE; PS00118; PA2 HIS; 1.
 KW Hydrolase; Lipid degradation; Signal; Calcium.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 168 GROUP IIF SECRETORY PHOSPHOLIPASE A2.
 FT ACT_SITE 67 67 BY SIMILARITY.
 FT ACT_SITE 114 114 BY SIMILARITY.
 FT DISULFID 46 138 BY SIMILARITY.
 FT DISULFID 48 64 BY SIMILARITY.
 FT DISULFID 63 120 BY SIMILARITY.
 FT DISULFID 69 145 BY SIMILARITY.
 FT DISULFID 70 113 BY SIMILARITY.
 FT DISULFID 79 106 BY SIMILARITY.
 FT DISULFID 98 111 BY SIMILARITY.
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
 (BY SIMILARITY).

```

FT METAL 49 49 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 51 51 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 68 68 CALCIUM (BY SIMILARITY)
SQ SEQUENCE 168 AA; 19880 MW; 9E15FB6AC0F5450C CRC64;
Query Match 39.4%; Score 336; DB 1; Length 168;
Best Local Similarity 42.8%; Pred. No. 5.8e-27;
Matches 62; Conservative 23; Mismatches 52; Indels 8; Gaps 4;
QY 3 LALLGLVVMAGVPIQGGILNLKMKVQVTKMPILSWPYCHGCLGGRGQPKDATDW 62
Db 7 IAVLAGSVTTA-----HSSLNLKSMVEAITHRNSILSFVGYCYGLGGRGHMPDEVDM 62
QY 63 CQOTHCDCYDHLTKTQCGYIKYRYNFSQGN-IHCSN-KGSCEQOLCACDKVEAFCLK 120
Db 63 CCHAHDCYCEKLEFQCGRPVVDYHRIENGWIVCTELNETCDKQTCEDCKSLTCLCK 122
QY 121 RNLDTYQKRLRFWRPHCRGTGPGC 145
Db 123 DH--PYRNKRYGFYNYCQGTENC 145

RESULT 12
PA2B CRODU
ID PA2B CRODU STANDARD; PRT; 138 AA.
AC 01-APR-1988 (Rel. 07, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phospholipase A2 CBI precursor (EC 3.1.1.4) (Crotoxin basic chain 1)
DE (Mojave toxin basic chain) (Mx-b) (phosphatidylcholine 2-acylhydrolase).
OS Crotoalus durissus terrificus (South American rattlesnake), and
OS Crotoalus scutulatus scutulatus (Mojave rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8732, 8738;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=C.d.terrificus; TISSUE=Venom gland;
RX MEDLINE=89016587; PubMed=3174444;
RA Ducancel F., Guignery Prelat G., Menez A., Boulain J.-C., Bouchier C., Bon C.;
RT "Cloning and sequencing of cDNAs encoding the two subunits of Crotoxin."
RL Nucleic Acids Res. 16:9050-9050(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=C.s.scutulatus; TISSUE=Liver;
RX MEDLINE=94156205; PubMed=8112610;
RA John T.R., Smith L.A., Kaiser I.I.;
RT "Genomic sequences encoding the acidic and basic subunits of Mojave toxin: unusually high sequence identity of non-coding regions."
RL Gene 139:229-234(1994).
RN [3]
RP SEQUENCE OF 17-138.
RC SPECIES=C.d.terrificus;
RX MEDLINE=86321989; PubMed=3753003;
RA Aird S.D., Kaiser I.I., Lewis R.V., Kruggel W.G.;
RT "A complete amino acid sequence for the basic subunit of crotoxin."
RL Arch. Biochem. Biophys. 249:296-300(1986).
RN [4]
RP SEQUENCE OF 17-138.
RC SPECIES=C.s.scutulatus; TISSUE=Venom;
RX MEDLINE=90385490; PubMed=2402763;
RA Aird S.D., Kruggel W.G., Kaiser I.I.;
RT "Amino acid sequence of the basic subunit of Mojave toxin from the venom of the Mojave rattlesnake (Crotoalus s. scutulatus)."
RL Toxicon 28:669-673(1990).
RN [5]

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RP SEQUENCE OF 17-49.
RC SPECIES=C.d.terrificus; TISSUE=Venom;
RX MEDLINE=94307256; PubMed=8033889;
RA Faure G., Choumet V., Bouchier C., Camoin L., Guillaume J.-L., Monegier B., Vuilhorgne M., Bon C.;
RT "The origin of the diversity of crotoxin isoforms in the venom of Crotoalus durissus terrificus."
RL Eur. J. Biochem. 223:161-164(1994).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. Inhibits neuromuscular transmission by blocking acetylcholine release from the nerve termini. Acts presynaptically.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBUNIT: This toxin consists of 2 subunits: acidic and basic. The acidic subunit is nontoxic, without enzymatic activity and comprises 3 peptides that are crosslinked by 7 disulfide bridges. The basic subunit is toxic, has phospholipase A2 activity and is composed of a single chain.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.

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EMBL; X12603; CAA311123.1; -
EMBL; U01027; AAC59674.1; -
PIR; I51381; I51381.
PIR; S02257; PSRSBT.
HSP; P14421; IAZA.
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_His; 1.
Lipid degradation; Hydrolase; Toxin; Neurotoxin;
Presynaptic neurotoxin; Calcium; Signal; Multigene family.
SIGNAL 1 16
CHAIN 17 138 PHOSPHOLIPASE A2 CBI.
FT ACT_SITE 63 63 BY SIMILARITY.
FT ACT_SITE 105 105 BY SIMILARITY.
FT DISULFID 42 131 BY SIMILARITY.
FT DISULFID 44 60 BY SIMILARITY.
FT DISULFID 59 111 BY SIMILARITY.
FT DISULFID 65 138 BY SIMILARITY.
FT DISULFID 66 104 BY SIMILARITY.
FT DISULFID 73 97 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT METAL 43 43 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 45 45 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 64 64 CALCIUM (BY SIMILARITY).
FT CONFLICT 81 81 P -> R (IN REF. 3).
SQ SEQUENCE 138 AA; 15907 MW; 84A118931DFFE2E3 CRC64;

```

Query Match 39.4%; Score 335.5; DB 1; Length 138;
Best Local Similarity 46.3%; Pred. No. 5.3e-27;
Matches 63; Conservative 18; Mismatches 52; Indels 3; Gaps 2;

QY 10 VVMAGVPIQGGILNLKMKVQVTKMPILSWPYCHGCLGGRGQPKDATDWCCCTHDC 69

Db 6 I V A V L L V G V E G H L L Q R K M I K E T R K N A I P F Y A F Y G C Y G W G R G R K P K D A T D R C C F V H D C 65
 QY 70 C Y D H L K T Q G G I Y K D Y R Y N F S G N I H C S D K S W C E Q L C A C K E V A F C L K R N L D T Y Q K R 129
 Db 66 C Y G - K L A K N T K W D I P Y S L K S G Y I T C G - K G T W C B E Q I C E C D R V A A E C L R S L S T Y K Y G 122
 QY 130 L R F Y W R P H C R G Q T P G C 145
 Db 123 Y M E Y P D S R C R G P S E T C 138

RESULT 13
 PA2W TRIFL STANDARD; PRT; 138 AA.
 AC Q02517;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Phospholipase A2 isozyme PL-X' precursor (EC 3.1.1.4)
 DE (Phosphatidylcholine 2-acylhydrolase).
 OS Trimeresurus flavoviridis (Habu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=88087;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Venom gland;
 RX MEDLINE=92409555; PubMed=1528861;
 RA Ogawa T., Oda N., Nakashima K.-I., Sasaki H., Hattori M., Sasaki Y.,
 RA Kinara H., Ohno M.;
 RT "Unusually high conservation of untranslated sequences in cDNAs for
 RT Trimeresurus flavoviridis phospholipase A2 isozymes."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8557-8561(1992).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the
 CC 2-acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
 CC subfamily.

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 or send an email to license@isb-sib.ch).

EMBL; D10721; BAA01564.1; -;
 DR HSP; P51972; IYAP.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR PRINTS; PR00389; PHPLIPASEA2.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR SMART; SM00085; PA2C; 1.
 DR PROSITE; PS00119; PA2 ASP; 1.
 DR PROSITE; PS00118; PA2 HIS; 1.
 KW Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 138 PHOSPHOLIPASE A2 ISOZYME PL-X'.
 FT ACT_SITE 63 63 BY SIMILARITY.
 FT ACT_SITE 105 105 BY SIMILARITY.
 FT DISULFID 42 131 BY SIMILARITY.
 FT DISULFID 44 60 BY SIMILARITY.
 FT DISULFID 59 111 BY SIMILARITY.
 FT DISULFID 65 138 BY SIMILARITY.
 FT DISULFID 66 104 BY SIMILARITY.
 FT DISULFID 73 97 BY SIMILARITY.

FT DISULFID 91 102 BY SIMILARITY.
 FT METAL 43 43 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 45 45 (BY SIMILARITY).
 FT METAL 45 45 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 47 47 (BY SIMILARITY).
 FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 64 64 (BY SIMILARITY).
 FT METAL 64 64 CALCIUM (BY SIMILARITY).
 SQ SEQUENCE 138 AA; 15733 MW; 471B01878CCAIED1 CRC64;
 Query Match 39.0%; Score 332; DB 1; Length 138;
 Best Local Similarity 46.3%; Pred. No. 1.2e-26;
 Matches 63; Conservative 19; Mismatches 48; Indels 6; Gaps 3;
 QY 10 V M A G V I P I Q G G I L N L N K M V K V T G K M P I L S Y P Y G C H L G R G Q P K D A T D R C C F V H D C 69
 Db 9 V L L V G V - - - E G H L L Q R K M I K K M T G K E P I V S Y A F Y G C Y G W G R G R K P K D A T D R C C F V H D C 65
 QY 70 C Y D H L K T Q G G I Y K D Y R Y N F S G N I H C S D K S W C E Q L C A C K E V A F C L K R N L D T Y Q K R 129
 Db 66 C Y E - - K V T G C D P R K W D I Y T S S E N G D I V C G G D N P - C Y K E V C E C D K A A A I C F R D N L K T Y K R 122
 QY 130 L R F Y W R P H C R G Q T P G C 145
 Db 123 Y M E Y P D I F C T D P T E K C 138
 RESULT 14
 PA2C CRODU STANDARD; PRT; 138 AA.
 AC P24027;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Phospholipase A2 CB2 precursor (EC 3.1.1.4) (Crotoxin basic chain 2)
 DE (Phosphatidylcholine 2-acylhydrolase).
 OS Crotalus durissus terrificus (South American rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8732;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Venom gland;
 RX MEDLINE=91198145; PubMed=2015302;
 RA Bouchier C., Boulain J.-C., Bon C., Menez A.;
 RT "Analysis of cDNAs encoding the two subunits of crotoxin, a
 RT phospholipase A2 neurotoxin from rattlesnake venom: the acidic non
 RT enzymatic subunit derives from a phospholipase A2-like precursor.";
 RL Biochim. Biophys. Acta 1088:401-408(1991).
 [2]
 RN SEQUENCE OF 17-49.
 RP TISSUE=Venom;
 RX MEDLINE=94307256; PubMed=8033889;
 RA Faure G., Choumet V., Bouchier C., Camoin L., Guillaume J.-L.,
 RA Monégier B., Vuilhorgne M., Bon C.;
 RT "The origin of the diversity of crotoxin isoforms in the venom of
 RT Crotalus durissus terrificus."
 RL Eur. J. Biochem. 223:161-164(1994).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides. Inhibits neuromuscular
 CC transmission by blocking acetylcholine release from the nerve
 CC termini. Acts presynaptically.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBUNIT: Crotoxin consists of 2 subunits: CA and CB. CA is acidic,
 CC nontoxic, without enzymatic activity and comprises 3 peptides that
 CC are crosslinked by 7 disulfide bridges. CB is basic, toxic, has
 CC phospholipase A2 activity and is composed of a single chain.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
 CC subfamily.

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DR EMBL; X16100; CAA34227.1; -;
 DR PIR; S15068; PRRS2.
 DR HSSP; P14421; 1A2A.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR PRINTS; PR00389; PHPLIPASEA2.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR SMART; SM00085; PA2C; 1.
 DR PROSITE; PS00119; PA2 ASP; 1.
 DR PROSITE; PS00118; PA2 HIS; 1.
 KW Hydrolase; Lipid degradation; Calcium; Signal; Multigene family.
 FT SIGNAL 1 16
 FT CHAIN 17 138 PHOSPHOLIPASE A2 CB2.
 FT ACT_SITE 63 63 BY SIMILARITY.
 FT ACT_SITE 105 105 BY SIMILARITY.
 FT DISULFID 42 131 BY SIMILARITY.
 FT DISULFID 44 60 BY SIMILARITY.
 FT DISULFID 59 111 BY SIMILARITY.
 FT DISULFID 65 138 BY SIMILARITY.
 FT DISULFID 66 104 BY SIMILARITY.
 FT DISULFID 73 97 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT METAL 43 43 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 45 45 (BY SIMILARITY).
 FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
 FT METAL 64 64 (BY SIMILARITY).
 FT METAL 64 64 CALCIUM (VIA CARBONYL OXYGEN)
 FT SEQUENCE 138 AA; 15968 MW; 935D12258D47B058 CRC64;
 Query Match 38.9%; Score 331.5; DB 1; Length 138;
 Best Local Similarity 44.1%; Pred. No. 1.3e-26;
 Matches 60; Conservative 21; Mismatches 52; Indels 3; Gaps 2;
 QY 10 VMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGGLGRGQPKDADTWCQTHDC 69
 Db 6 IVALLVGVGSLFELGKMTWQETGKNPVKNYGLYGCNGVGRGFLDATDRCCFVHDC 65
 QY 70 CYDHLKTQGGIYKDYRYNFSQGNTHCSDKGSWCEQQLCACDKEVAFCLKRLNLDITYQKR 129
 Db 66 CYG--KLAKNTKWDIYRSLKSGYITCG-KGTWCKEQICECDRAAECLRRSLSTYKNE 122
 QY 130 LRFYWRPHCRGQTGPGC 145
 Db 123 YMFYDPSRCRPSPTC 138

RESULT 15
 ID PA2H AGKAC STANDARD; PRT; 138 AA.
 AC OS7385; Q8UVZ5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Phospholipase A2 homolog Dac-K491I precursor.
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Deinagkistrodon.
 OX NCBI_TaxID=36307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;

RX MEDLINE=99183869; PubMed=10084123;
 RA Fan C.Y., Qian Y.C., Yang S.L., Gong Y.;
 RT "cDNA cloning and sequence analysis of Lys-49 phospholipase A2 from
 RT Agkistrodon acutus.";
 RL Genet. Anal. 15:15-18(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=21478853; PubMed=11594738;
 RA Tsai I.-H., Chen Y.-H., Wang Y.-M., Tu M.-C., Tu A.T.;
 RT "Purification, sequencing, and phylogenetic analyses of novel Lys-49
 RT phospholipases A(2) from the venoms of rattlesnakes and other pit
 RT vipers.";
 RL Arch. Biochem. Biophys. 394:236-244(2001).
 CC -!- FUNCTION: Myotoxic protein that lacks PA2 enzymatic activity.
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MISCELLANEOUS: Does not bind calcium as one of the calcium binding
 CC ligands is lost (Asp->Lys in position 64).
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
 CC subfamily.

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DR EMBL; AJ223188; CAA11159.1; -;
 DR EMBL; AF269132; AAL36975.1; -;
 DR PDB; IMC2; 2I-AUG-02.
 DR PDB; IMG6; 04-SEP-02.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR PRINTS; PR00389; PHPLIPASEA2.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR SMART; SM00085; PA2C; 1.
 DR PROSITE; PS00119; PA2 ASP; 1.
 DR PROSITE; PS00118; PA2 HIS; 1.
 KW Toxin; Signal; 3D-structure.
 FT SIGNAL 1 16 BY SIMILARITY.
 FT CHAIN 17 138 PHOSPHOLIPASE A2 HOMOLOG DAC-K491I.
 FT ACT_SITE 63 63 BY SIMILARITY.
 FT ACT_SITE 105 105 BY SIMILARITY.
 FT DISULFID 42 131 BY SIMILARITY.
 FT DISULFID 44 60 BY SIMILARITY.
 FT DISULFID 59 111 BY SIMILARITY.
 FT DISULFID 65 138 BY SIMILARITY.
 FT DISULFID 66 104 BY SIMILARITY.
 FT DISULFID 73 97 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT DISULFID 130 130 S->L (IN REF. 2).
 FT CONFLICT 130 130
 FT SEQUENCE 138 AA; 15777 MW; 1353CD8C8F54DA99 CRC64;
 Query Match 38.8%; Score 330.5; DB 1; Length 138;
 Best Local Similarity 43.4%; Pred. No. 1.7e-26;
 Matches 59; Conservative 21; Mismatches 53; Indels 3; Gaps 2;
 QY 10 VMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHGGLGRGQPKDADTWCQTHDC 69
 Db 6 IVALLVGVGSLFELGKMTWQETGKNPVKNYGLYGCNGVGRGFLDATDRCCFVHDC 65
 QY 70 CYDHLKTQGGIYKDYRYNFSQGNTHCSDKGSWCEQQLCACDKEVAFCLKRLNLDITYQKR 129
 Db 66 CYG--KLTKDCKKDRYSYKWKNAIVCG-KNQPCQEMCECDKAFACLRLNLDITYNKS 122
 QY 130 LRFYWRPHCRGQTGPGC 145
 Db 123 FRYHLKPSCKTSEQC 138

us-09-830-321a-1.rsp

Fri Oct 8 10:22:31 2004

Search completed: October 5, 2004, 19:25:30
Job time : 6.8 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 18:51:24 ; Search time 28.8067 Seconds
(without alignments)
1588.179 Million cell updates/sec

Title: US-09-830-321A-1
Perfect score: 852
Sequence: 1 MELALLGLVVMAGVPIQG.....YQKRLRFYWRPHCRGQTGFC 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL_25.*
- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rviro.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	400.5	47.0	146	11 Q91Y34	Q91Y34 rattus norv
2	389	45.7	154	11 Q9QX68	Q9QX68 mesocricetu
3	352	41.3	168	4 Q8N217	Q8N217 homo sapien
4	347	40.7	187	4 Q8N435	Q8N435 homo sapien
5	336	39.4	210	11 Q8CE14	Q8CE14 mus musculus
6	334	39.2	137	13 Q804D7	Q804D7 bothrops ja
7	330	38.7	202	11 Q8BJ93	Q8BJ93 mus musculus
8	314	36.9	138	13 Q805A3	Q805A3 trimeresuru
9	312.5	36.7	136	13 Q7T3S7	Q7T3S7 echis carin
10	309	36.3	138	13 Q805A2	Q805A2 trimeresuru
11	306.5	36.0	138	13 Q7T1D5	Q7T1D5 vipera beru
12	296.5	34.8	150	11 Q8K0Y1	Q8K0Y1 mus musculus
13	295.5	34.7	138	13 Q7Z2Q1	Q7Z2Q1 vipera russ
14	294	34.5	138	13 Q8AXY1	Q8AXY1 bothrops ja
15	289.5	34.0	138	13 Q7T1C6	Q7T1C6 vipera aspi
16	283.5	33.3	138	13 Q7T2R1	Q7T2R1 vipera russ

17	274.5	32.2	138	13 Q7T1D1	Q7T1D1 vipera beru
18	269.5	31.6	138	13 Q7T1D4	Q7T1D4 vipera aspi
19	269.5	31.6	138	13 Q7T1D3	Q7T1D3 vipera aspi
20	269.5	31.6	138	13 Q7T1D2	Q7T1D2 vipera aspi
21	261.5	30.7	138	13 Q800C2	Q800C2 crotalus vi
22	260.5	30.6	138	13 Q800C4	Q800C4 crotalus vi
23	260.5	30.6	138	13 Q800C1	Q800C1 crotalus vi
24	259.5	30.5	138	13 Q7ZTA7	Q7ZTA7 crotalus vi
25	255.5	30.0	138	13 Q800C3	Q800C3 crotalus vi
26	255.5	30.0	141	11 Q8C5Y6	Q8C5Y6 mus musculu
27	251.5	29.5	130	13 Q7T3T5	Q7T3T5 vipera russ
28	246	28.9	138	13 Q7ZTA8	Q7ZTA8 crotalus vi
29	244	28.6	138	13 Q7ZTA6	Q7ZTA6 crotalus vi
30	234	27.5	147	13 Q7ZM60	Q7ZM60 rana catesb
31	222.5	26.1	147	13 Q7T2Q5	Q7T2Q5 bungarus fl
32	221.5	26.0	156	5 Q8WS88	Q8WS88 adamsia car
33	218.5	25.6	147	13 Q7T2Q4	Q7T2Q4 bungarus fl
34	210.5	24.7	146	13 Q7T1R0	Q7T1R0 bungarus fl
35	208	24.4	142	13 Q802I1	Q802I1 bungarus ca
36	199	23.4	453	11 Q80ZM2	Q80ZM2 mus musculu
37	198.5	23.3	146	13 Q8AXW2	Q8AXW2 bungarus mu
38	197.5	23.2	144	11 Q8K130	Q8K130 mus musculu
39	196.5	23.1	145	13 Q8AXW0	Q8AXW0 bungarus mu
40	196	23.0	149	13 Q9YH62	Q9YH62 dicentrarch
41	196	23.0	149	13 Q57313	Q57313 pagrus majo
42	192.5	22.6	167	5 Q86DU7	Q86DU7 polyandroca
43	192	22.5	177	5 Q8IML0	Q8IML0 drosophila
44	189.5	22.2	146	13 Q8AXW7	Q8AXW7 micrurus co
45	189	22.2	137	13 Q8AY48	Q8AY48 bungarus ca

ALIGNMENTS

RESULT 1

Q91Y34	PRELIMINARY;	PRT;	146 AA.
ID Q91Y34			
AC Q91Y34			
DT 01-DEC-2001 (TRENBLrel. 19, Created)			
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)			
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)			
DE Platelet phospholipase A2 precursor (Fragment).			
OS Rattus norvegicus (Rat)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX NCBI_TaxID=10116;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=Wistar; TISSUE=Blood;			
RA Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.;			
RT "Cloning and sequence determination of rat platelet phospholipase A2			
RT from whole blood."			
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AF365363; AAK52061.1; -			
DR GO; GO:0005509; F:calcium ion binding; IEA.			
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.			
DR GO; GO:0016042; F:lipid catabolism; IEA.			
DR InterPro; IPR001211; PhospholipaseA2.			
DR Pfam; PF00068; phoslip; 1.			
DR PRINTS; PR00389; PPHPLIPASEA2.			
DR ProDom; PD000303; PhospholipaseA2; 1.			
DR SMART; SM00085; PA2c; 1.			
DR PROSITE; PS00119; PA2_ASP; 1.			
DR PROSITE; PS00118; PA2_HIS; 1.			
KW SIGNAL.			
FT SIGNAL	1	21	POTENTIAL.
FT CHAIN	22	>146	PLATELET PHOSPHOLIPASE A2.
FT NON_TER	146	146	
SQ SEQUENCE	146 AA;	16306 MW;	60C1C9EC85DCBD67 CRC64;

Query Match 47.0%; Score 400.5; DB 11; Length 146;
Best Local Similarity 47.9%; Pred. No. 3e-38;
Matches 70; Conservative 23; Mismatches 52; Indels 1; Gaps 1;

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QY 1 MELALLCGLVMA-GVPIQGGILNLNMKVQVTKMPILSYWPGYCHGGLGGRGPKDA 59
Db 1 MKVLLLAIVVIMAFSGIQVQSGLLFQCFKTRADSYGYFGYCHGGLGGRGSPKDA 60
QY 60 TDWCCQTHDCYDHLKTCGGGDIYKYRNFYSQNIHCSKGSWCEQQQLCACDKEVAFCL 119
Db 61 TDWCCVTHDCYRLEKRGGKTLTYKFSYRGGRISCSINQDSCKQLCQCDKAAAEFCF 120
QY 120 KRLNDTYQKRLRFYWRPHRCGQTGPGC 145
Db 121 ARNKKSYSLSKYQFYFNKFCGKGTGPGC 146

RESULT 2
Q9QX68 PRELIMINARY; PRT; 154 AA.
ID Q9QX68;
AC Q9QX68;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Src-associated phospholipase A2 precursor (EC 3.1.1.4).
GN SRPLA2.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN SEQUENCE FROM N.A.
RP TISSUE=Fibroblast;
RA Mirenia O., Musatkin E., Yanushevich V., Rodina A., Krasilnikov M.,
RA De Gunzburg J., Camonis J., Tavitian A., Tatosyan A.;
RT "A novel group IIA phospholipase A2 interacts with v-Src oncoprotein
RT from RSV-transformed hamster cells.";
RL J. Biol. Chem. 27606:34006-34012(2001).
DR EMBL; AJ251361; CAB62564.1; -.
DR HSSP; P14555; 1POD.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004627; F:calcium-dependent cytosolic phospholipase A. .; IEA.
DR GO; GO:0004625; F:calcium-independent secreted phospholipase A2. .; IEA.
DR GO; GO:0004628; F:calcium-independent cytosolic phospholipase. .; IEA.
DR GO; GO:0004626; F:cytosolic phospholipase A2 activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0004624; F:secreted phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2 HIS; 1.
KW Hydrolase; Signal.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE 154 AA; 17217 MW; F5E0A76CE441772C CRC64;
QY 3 LALLCGLVMAGVPIQGGILNLNMKVQVTKMPILSYWPGYCHGGLGGRGPKDATDW 62
Db 4 LLLALLNVFPIQIQGSLAEINLMWLTQWRAGLSTVAFYCHGGLGGRGSPKDATDW 63
QY 63 CCQTHDCYDHLKTCGGGDIYKYRNFYSQNIHCSKGSWCEQQQLCACDKEVAFCLKN 122
Db 64 CCAAHDCYDRLDLGCGTKSLDYNFKYSRGTEITCSVNDQFCGQQLCHCDRLAECLAQH 123
QY 123 LDTYQKRLRFYWRPHRCGQTGPGC 145

Query Match 45.7%; Score 389; DB 11; Length 154;
Best Local Similarity 48.3%; Pred. No. 6.7e-37;
Matches 69; Conservative 21; Mismatches 53; Indels 0; Gaps 0;

QY 3 LALLCGLVMAGVPIQGGILNLNMKVQVTKMPILSYWPGYCHGGLGGRGPKDATDW 62
Db 4 LLLALLNVFPIQIQGSLAEINLMWLTQWRAGLSTVAFYCHGGLGGRGSPKDATDW 63
QY 63 CCQTHDCYDHLKTCGGGDIYKYRNFYSQNIHCSKGSWCEQQQLCACDKEVAFCLKN 122
Db 64 CCAAHDCYDRLDLGCGTKSLDYNFKYSRGTEITCSVNDQFCGQQLCHCDRLAECLAQH 123
QY 123 LDTYQKRLRFYWRPHRCGQTGPGC 145

Query Match 41.3%; Score 352; DB 4; Length 168;
Best Local Similarity 45.5%; Pred. No. 1.4e-32;
Matches 66; Conservative 19; Mismatches 52; Indels 8; Gaps 4;

QY 3 LALLCGLVMAGVPIQGGILNLNMKVQVTKMPILSYWPGYCHGGLGGRGPKDATDW 62
Db 7 VALLAGSVLSTA---HGSLLNLKAMVAEVTGSRSAISLVGVGYCYGGLGGRGPKDEVDW 62
QY 63 CCQTHDCYDHLKTCGGGDIYKYRNFYSQNIHCSKGSWCEQQQLCACDKEVAFCLK 120
Db 63 CCAAHDCYQELFDQGCHPYVDHTIENNTIYVCSLNTKTECDKQTCMDCKNMVLCML 122
QY 121 RNLDTYQKRLRFYWRPHRCGQTGPGC 145
Db 123 N--QTYREYRGLNVCQGTGPGC 145

RESULT 4
Q8N435 PRELIMINARY; PRT; 187 AA.
ID Q8N435;
AC Q8N435;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC Strausberg R.;

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RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036792; AAH36792.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 187 AA; 20811 MW; 2DAA2274359A3A60 CRC64;

  Query Match      40.7%; Score 347; DB 4; Length 187;
  Best Local Similarity 43.6%; Pred. No. 6e-32;
  Matches 58; Conservative 27; Mismatches 36; Indels 12; Gaps 2;

QY 12 MAGVIP-----IQGGILNLNKMVKQVTGKMPILSYWPGYCHGGLGGRGPKDAT 60
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 50 MKGLPLAWFLACSPVAVQGLLDLKSMEKVTGKNAITNYGYCYCGWGRGTPKDG 109
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 61 DWCCQTHDCCYDHLTKTQCGGIYKYDYRNFSGNHCSDKGSWCQQLCACDKEVAFCLK 120
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 110 DWCCWAHDHCYGRLEKGNRTQSKYRFANGVVC-EPGPFCHVNLCACDKLVYCLK 168
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 121 RNLDTYQKRLRFY 133
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 169 RNLSYNPQYQYF 181
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 5
Q8CE14 PRELIMINARY; PRT; 210 AA.
AC Q8CE14;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Phospholipase A2.
GN PLA2G2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK029254; BAC26357.1; -.
DR MGD; MGI:1349660; Pla2g2b.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 210 AA; 23259 MW; 5AC55CD96F68FC28 CRC64;

  Query Match      39.4%; Score 336; DB 11; Length 210;
  Best Local Similarity 42.8%; Pred. No. 1.3e-30;
  Matches 62; Conservative 23; Mismatches 52; Indels 8; Gaps 4;

QY 3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPGYCHGGLGGRGPKDATW 62
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPGYCHGGLGGRGPKDATW 62
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPGYCHGGLGGRGPKDATWCCQTHDC 69
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 9 VLVGVV---EGSLFEFGKMTLQETGNPKASYGAYGNCVGLGKPKDATDRCCYVHKC 65
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 70 CYDHLTKTQCGGIYKYDYRNFSGNHCSDKGSWCQQLCACDKEVAFCLKRLNLDTYQKR 129
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 66 CYK--KLTCGDPKDRYSYKDKTIVCGNNP-CLKELCECDKVAICURENLGTNKK 122
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Db 49 IAVLAGSVVTTA----HSLLNLMKSMVEAITHRNSILTSFVGCGYCGLGGRGHPMDVDW 104
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 63 CCQTHDCCYDHLTKTQCGGIYKYDYRNFSGN- IHCSD-KGSWCQQLCACDKEVAFCLK 120
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 105 CCHAHDCCYCKLFEQGRPYVDHRIENGTMIVCTELNETECQKQTCCECKSLTLCLK 164
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 121 RNLDTYQKRLRFYWRPHRCGQTPGC 145
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 165 DH--PYRNKYGYFNVCQGPENC 187
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 6
Q804D7 PRELIMINARY; PRT; 137 AA.
AC Q804D7;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Myotoxic phospholipase A2-like (Myotoxic A2-like phospholipase).
OS Bothrops jararacussu (Jararacussu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8726;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20472069; PubMed=11018293;
RA Andriao-Escarso S.H., Soares A.M., Rodrigues V.M., Angulo Y., Diaz C.,
RA Lomonte B., Gutierrez J.M., Giglio J.R.;
RT "Myotoxic phospholipases A(2) in bothrops snake venoms: effect of
RT chemical modifications on the enzymatic and pharmacological properties
RT of bothropstoxins from Bothrops jararacussu.";
RL Biochimie 82:755-763 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Kashima S., Soares A.M., Roberto P.G., Astolfi-Filho S., Pereira J.O.,
RA Silva M.X., Guillati S., Farias M. Jr., Giglio J.R., Franca S.C.;
RT "Analysis of Bothrops jararacussu Venomous Gland Transcriptome with
RT Structural and Functional Categories: Gene Expression Profile of
RT Phospholipases A2."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Hayashi M.A.F., Queiroz G.P., Radis-Baptista G., Yamane T.,
RA Camargo A.C.M.;
RT "Bothrops jararacussu myotoxic phospholipase A2-like mRNA.";
RL EMBL; AY185200; AA027453.1; -.
DR EMBL; AY299391; AAP57527.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 137 AA; 15497 MW; 7BE006BABC4DFC39 CRC64;

  Query Match      39.2%; Score 334; DB 13; Length 137;
  Best Local Similarity 46.3%; Pred. No. 1.4e-30;
  Matches 62; Conservative 19; Mismatches 47; Indels 6; Gaps 3;

QY 10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPGYCHGGLGGRGPKDATWCCQTHDC 69
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 9 VLVGVV---EGSLFEFGKMTLQETGNPKASYGAYGNCVGLGKPKDATDRCCYVHKC 65
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 70 CYDHLTKTQCGGIYKYDYRNFSGNHCSDKGSWCQQLCACDKEVAFCLKRLNLDTYQKR 129
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 66 CYK--KLTCGDPKDRYSYKDKTIVCGNNP-CLKELCECDKVAICURENLGTNKK 122
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Fri Oct 8 10:22:32 2004

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QY 130 LRFYWRPHCRGQTP 143
DB 123 YRYHLKPFCKKADP 136

RESULT 7
Q805A3 PRELIMINARY; PRT; 202 AA.
AC Q805A3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium-dependent phospholipase A2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; PubMed=12466851;
RX MEDLINE=22354683;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK090021; BAC41050.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PRO0389; PHEHLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 202 AA; 22770 MW; BDBA97C09F64F7C4 CRC64;

Query Match 38.7%; Score 330; DB 11; Length 202;
Best Local Similarity 44.3%; Pred. No. 6.1e-30;
Matches 58; Conservative 24; Mismatches 43; Indels 6; Gaps 2;

QY 8 GLVWMA-----GVPIQGIILNLMKWKQVTGKMPILSYWPGCHGCGRGQPKDATDW 62
DB 3 GLLTLAWFLACSVPAVPGGLLELKSIEKVTGNKAFNYGFCYCGWGGRTPKDGTW 62

QY 63 CQOHDCCYDHLKTQCGGIYKDYRYNFSQGNHSCDKGSWCEQQIACDKEVAFCLRN 122
DB 63 CQOHDCCYDHLKTQCGGIYKDYRYNFSQGNHSCDKGSWCEQQIACDKEVAFCLRN 122

QY 123 LDTYQKRLRFY 133
DB 122 LWTYNPLFYQY 132

RESULT 8
Q805A3 PRELIMINARY; PRT; 138 AA.
AC Q805A3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phospholipase A2.
GN PLA-N.
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
CX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.

RA Chijiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,
RA Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.;
RT "Interisland mutation of a novel phospholipase A2 from Trimeresurus
RT flavoviridis venom and evolution of crotalinae group II phospholipase
RT A2."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB102728; BAC56892.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PRO0389; PHEHLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
SQ SEQUENCE 138 AA; 15617 MW; A2F7B5A23897ECC5 CRC64;

Query Match 36.9%; Score 314; DB 13; Length 138;
Best Local Similarity 44.9%; Pred. No. 2.8e-28;
Matches 61; Conservative 19; Mismatches 50; Indels 6; Gaps 3;

QY 10 VVMAGVPIQGIILNLMKWKQVTGKMPILSYWPGCHGCGRGQPKDATDWCCQTHDC 69
DB 9 VLLGVG---EGLLQFNKMKIMTKNGFFPYTSYCYCGWGGRGKPKDATDRCCFVHDC 65

QY 70 CYDHLKTQCGGIYKDYRYNFSQGNHSCDKGSWCEQQIACDKEVAFCLRNLDTYQKR 129
DB 66 CYE--KLTDSPKSDIYSYWKTVGICG--GTECEKQICEDRAAAVCFQGLRTYKKK 122

QY 130 LRFYWRPHCRGQTPGC 145
DB 123 YMFYDFELCTDPTKTC 138

RESULT 9
Q7T3S7 PRELIMINARY; PRT; 136 AA.
AC Q7T3S7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4).
OS Echin carinatus (Saw-scaled viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Echis.
CX NCBI_TaxID=40353;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Jasti J., Murugan P., Alagiri S., Singh T.P.;
RT "X-ray structure of acidic phospholipase A2 from Indian saw-scaled-
RT viper (Echis carinatus) with a potent platelet aggregation inhibition
RT activity."
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY268946; AAP41217.1; -.
KW Hydrolase.
SQ SEQUENCE 136 AA; 15523 MW; 39699DA1D01271BA CRC64;

Query Match 36.7%; Score 312.5; DB 13; Length 136;
Best Local Similarity 41.2%; Pred. No. 4.2e-28;
Matches 56; Conservative 22; Mismatches 53; Indels 5; Gaps 3;

QY 10 VVMAGVPIQGIILNLMKWKQVTGKMPILSYWPGCHGCGRGQPKDATDWCCQTHDC 69
DB 6 IVAVMLIAVEGMLYQFGRMINWRTGKLPILSYGSGYCGWGGQGPDKDATDRCCLVHDC 65

QY 70 CYDHLKTQCGGIYKDYRYNFSQGNHSCDKGSWCEQQIACDKEVAFCLRNLDTYQKR 129
DB 66 CY--TRVGDCSPKMTLYSYRFENGDIICDNKDP--CKRAVCECDREAAICLGENVNTYDKK 122
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AC Q7ZQ1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phospholipase A2-1.
OS Vipera russelli siamensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=228341;
RN [1]
RP SEQUENCE FROM N.A.
RA Yong-Hong J., Yang J., Run-Qiang C., Dong-Sheng L., Xing-Ding Z.,
RA Wan-Yu W., Yu-Liang X.;
RT "A novel phospholipase A2 from Vipera russelli siamensis: isolation,
RT cloning and sequence comparison.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY256974; AAP13805.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PPHLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR SEQUENCE 138 AA; 15401 MW; EB86AB8D46430DF3 CRC64;
SQ
Query Match 34.7%; Score 295.5; DB 13; Length 138;
Best Local Similarity 39.0%; Pred. No. 3.9e-26;
Matches 53; Conservative 23; Mismatches 57; Indels 3; Gaps 2;

Qy 10 VVMAGVPIQGGILNLNMVKQVTGKMPILSYWPVYCHGCGGRQPKDATDWCCQTHDC 69
Db 6 IVAVCLIGVEGNLYGFGEINQKTNFGLLSYVYCYCGWGGKGPQDATDRCCFVHDC 65

Qy 70 CYDHLKTQCGGYKYDYRYNFSQGNHCHSDKGSWCEQOLCACDKEVAFCLKRNLDYQKR 129
Db 66 CYG--TVNDCNPKMATYSYSPENGDIVCGD--NNLCLKTVCECDRAAAILCGQVNTYDN 122

Qy 130 LRFYWRPHCRGQTGTC 145
Db 123 YENYAISHCTESEQC 138

RESULT 14
Q8AXY1
ID Q8AXY1 PRELIMINARY; PRT; 138 AA.
AC Q8AXY1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypotensive phospholipase A2.
OS Bothrops jararacussu (Jararacussu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8726;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Venom gland;
RC TISSUE=Venom gland;
RX MEDLINE=22157211; PubMed=12167491;
RA Andrao-Escarso S.H., Soares A.M., Pontes M.R., Fuly A.L.,
RA Correa F.M., Rosa J.C., Greene L.J., Giglio J.R.;
RT "Structural and functional characterization of an acidic platelet
RT aggregation inhibitor and hypotensive phospholipase A(2) from Bothrops
RT jararacussu snake venom.";
RL Biochem. Pharmacol. 64:723-732(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Tissue=Venom gland;
RC TISSUE=Venom gland;

```

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RA Roberto P.G., Kashima S., Soares A.M., Astolfi-Filho S., Giglio J.R.,
RA Franca S.C.;
RT "Functional and Structural Analysis of Acidic and Basic Phospholipases
RT A2 from Bothrops jararacussu Snake Venom.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY45936; AAN37410.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PPHLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR SEQUENCE 138 AA; 15456 MW; 513647907BFD0F4E CRC64;
SQ
Query Match 34.5%; Score 294; DB 13; Length 138;
Best Local Similarity 39.7%; Pred. No. 5.8e-26;
Matches 54; Conservative 22; Mismatches 54; Indels 6; Gaps 3;

Qy 10 VVMAGVPIQGGILNLNMVKQVTGKMPILSYWPVYCHGCGGRQPKDATDWCCQTHDC 69
Db 9 VLLGVV---EGSLWQFGKMINYVMGESVLQYLSYCYCGLGQGGQPTDATDRCCFVHDC 65

Qy 70 CYDHLKTQCGGYKYDYRYNFSQGNHCHSDKGSWCEQOLCACDKEVAFCLKRNLDYQKR 129
Db 66 CYG--KVTGCDPKIDSYTSKNGDVVCGGDDP--CKQICECDRVATTTCFRDNKDTYDIK 122

Qy 130 LRFYWRPHCRGQTGTC 145
Db 123 YWFGAKNCOBKSEFC 138

RESULT 15
Q7T1C6
ID Q7T1C6 PRELIMINARY; PRT; 138 AA.
AC Q7T1C6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vaspin B isoform 1.
OS Vipera aspis aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=194601;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22707820; PubMed=12823540;
RA Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;
RT "Sequences and structural organization of phospholipase A2 genes from
RT Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom.
RT Identification of the origin of a new viper population based on
RT ammodytin II heterogeneity.";
RL Eur. J. Biochem. 270:2697-2706(2003).
DR EMBL; AY243575; AAO86503.1; -.
DR SEQUENCE 138 AA; 15550 MW; 28C749C004DE408E CRC64;
SQ
Query Match 34.0%; Score 289.5; DB 13; Length 138;
Best Local Similarity 39.0%; Pred. No. 1.9e-25;
Matches 53; Conservative 21; Mismatches 59; Indels 3; Gaps 2;

Qy 10 VVMAGVPIQGGILNLNMVKQVTGKMPILSYWPVYCHGCGGRQPKDATDWCCQTHDC 69
Db 6 IVAVCLIGVEGNLFOSAKMINKLGAPSVWNVISYCYCGWGGQGPDKDATDRCCFVHDC 65

Qy 70 CYDHLKTQCGGYKYDYRYNFSQGNHCHSDKGSWCEQOLCACDKEVAFCLKRNLDYQKR 129
Db 66 CYG--RVGCGNPKLAIYSYSPFKNGIVCG--KNGGCLRDICECDRVAANGFHQNTYKN 122

Qy 130 LRFYWRPHCRGQTGTC 145

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Fri Oct 8 10:22:32 2004

us-09-830-321a-1.rspt

Page 7

Db 123 YRFLSSRCRQTSQC 138

Search completed: October 5, 2004, 19:24:02
Job time : 30.8067 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 18:50:04 ; Search time 138.747 Seconds
(without alignments)
1232.039 Million cell updates/sec

Title: US-09-830-321A-2

Perfect score: 3235

Sequence: 1 MIFVLSPTLALCLERVASH.....EQLEALRQAVRRRRRPH 605

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_29Jan04.*

1: Genesep1980s.*

2: Genesep1980s.*

3: Genesep2000s.*

4: Genesep2001s.*

5: Genesep2002s.*

6: Genesep2003s.*

7: Genesep2003bs.*

8: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3235	100.0	605	3 AAB03628	Aab03628 Human pho
2	2767.5	85.5	778	5 AAU10696	Aau10696 Human CPL
3	2767.5	85.5	778	6 ABG76482	Abg76482 Human par
4	2767.5	85.5	797	5 AAU10697	Aau10697 CPLA2 N-t
5	2767.5	85.5	797	6 ABG76483	Abg76483 Human cyt
6	2767.5	85.5	913	3 AAY51557	Aay51557 Human PLA
7	2767.5	85.5	913	4 AAB74635	Aab74635 Phospholi
8	2767.5	85.5	913	4 AAB82415	Aab82415 Human pho
9	2767.5	85.5	533	3 AAB21140	Aab21140 Human cyt
10	2700	83.5	1020	4 ABG05871	Abg05871 Novel hum
11	2610.5	80.7	1040	4 ABG20154	Abg20154 Novel hum
12	2509.5	77.6	483	2 AAW75132	Aaw75132 Human sec
13	2509.5	77.6	483	2 AAW75067	Aaw75067 Human sec
14	2509.5	77.6	483	6 ABO01943	Ab001943 Novel hum
15	2509.5	77.6	483	6 ABO02008	Ab002008 Novel hum
16	1492	46.1	802	5 AAE22843	Aae22843 Human pho
17	1492	46.1	818	7 ADB61634	Adb61634 Human 818
18	1492	46.1	1026	5 ABB07497	Abb07497 Human lip
19	1492	46.1	1045	7 ADC10174	Adc10174 Human NOV
20	1455	45.0	1746	4 ABG05869	Abg05869 Novel hum
21	1243.5	38.4	996	5 ABB78290	Abb78290 Amino aci
22	1139.5	35.2	849	5 ABB09144	Abb09144 Human pho
23	1139.5	35.2	849	7 ADE08121	Ade08121 Novel pro
24	1138	35.2	853	5 ABB09149	Abb09149 Mouse pho
25	1127	34.8	854	5 ABB09147	Abb09147 Mouse pho

26	1123.5	34.7	1600	4 AAE05958	Aae05958 Human pho
27	1112	34.4	848	5 ABB07494	Abb07494 Human lip
28	1101.5	34.0	1624	4 AAE05956	Aae05956 Human pho
29	1031.5	31.9	798	5 AAE22833	Aae22833 Human pho
30	1022	31.6	1497	4 ABG20153	Abg20153 Novel hum
31	886.5	27.4	188	4 ABG20150	Abg20150 Novel hum
32	629.5	19.5	438	4 ABG20151	Abg20151 Novel hum
33	619	19.1	749	2 AAR26501	Aar26501 Cytosolic
34	619	19.1	749	2 AAR54090	Aar54090 PLA2 phos
35	619	19.1	749	2 AAR63757	Aar63757 Human pho
36	619	19.1	749	2 AAR97751	Aar97751 Human pho
37	619	19.1	749	2 AAW11607	Aaw11607 Human pho
38	619	19.1	749	2 AAW14650	Aaw14650 Human pho
39	619	19.1	749	3 AAY59631	Aay59631 Human pho
40	619	19.1	749	5 AAO15549	Aao15549 Human cyt
41	619	19.1	749	6 ABU03480	Abu03480 Angiogene
42	619	19.1	749	7 ADE62603	Ade62603 Human pro
43	616.5	19.1	611	3 AAB21142	Aab21142 Human cyt
44	611.5	18.9	749	5 AAE22834	Aae22834 Human pho
45	599.5	18.5	748	5 AAE23054	Aae23054 Human pho

ALIGNMENTS

RESULT 1
AAB03628
ID AAB03628 standard; protein; 605 AA.
XX
AC AAB03628;
XX
DT 05-OCT-2000 (first entry)
XX Human phospholipase 2 HPPL2.
DE Human phospholipase 2; HPPL2; cancer; autoimmune disorder;
KW inflammatory disorder; reproductive disorder; infection.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Modified-site 72
FT Modified-site /label= potential_phosphorylation_site
FT Modified-site 78
FT Modified-site /label= potential_phosphorylation_site
FT Modified-site 104
FT Modified-site /label= potential_phosphorylation_site
FT Modified-site 186
FT Modified-site /label= potential_phosphorylation_site
FT Modified-site 282
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FT Modified-site 293
FT Modified-site /label= potential_phosphorylation_site
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FT Modified-site /label= potential_glycosylation_site
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FT Modified-site 540
FT Modified-site /label= potential_phosphorylation_site
FT Modified-site 550
FT Modified-site /label= potential_glycosylation_site
FT Modified-site 552
FT Modified-site /label= potential_phosphorylation_site

Modified-site 566 /label= potential_phosphorylation_site

W0200024911-A2.

04-MAY-2000.

27-OCT-1999; 99WO-US025021.

27-OCT-1998; 98US-00181317.

21-JAN-1999; 99US-00234726.

(INCYTE-) INCYTE PHARM INC.

Hillman JL, Bandman O, Guegler KJ, Corley NC, Baughn MR, Azimzai Y, Lal P, Lu DAM;

WPI; 2000-350750/30.

N-PSDB; AAAS3270.

Human phospholipase genes and proteins useful to diagnose, prevent or treat cancer, autoimmune or inflammatory or reproductive disorders.

Disclosure; Page 71-72; 80pp; English.

The present sequence is human phospholipase 2 (HPL2). This protein is involved in the hydrolysis of membrane phospholipids. The protein and its coding sequence can be used to diagnose and treat the following: cancers such as prostate, breast and testicular cancers, autoimmune and inflammatory disorders such as AIDS, allergies, aneemia, asthma, atherosclerosis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, psoriasis, rheumatoid arthritis and systemic lupus erythematosus, infection caused by viruses, fungi, bacteria, parasites and protozoa, and reproductive disorders including infertility, disruptions of the menstrual cycle, polycystic ovary syndrome, ectopic pregnancies, disruptions of spermatogenesis, cancers within the reproductive tract and impotence

Sequence 605 AA;

Query Match 100.0%; Score 3235; DB 3; Length 605;

Best Local Similarity 100.0%; Pred. No. 4.3e-292;

Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MIFVELSPTALCLERVASHLTDGTLVLFPCAPCPFFPFEMESLSVAQGVQWRDLGS 60

1 MIFVELSPTALCLERVASHLTDGTLVLFPCAPCPFFPFEMESLSVAQGVQWRDLGS 60

61 LQPPPLGFRFSCLSLPSWDYRLRLAVRLGFGPCAEQAFLSRRKQVVAALRQALQ 120

61 LQPPPLGFRFSCLSLPSWDYRLRLAVRLGFGPCAEQAFLSRRKQVVAALRQALQ 120

121 DGDLODEIPVVAIMATGGIRAMTSLYQLAGLGLDCVYITGASGTWALANLY 180

121 DGDLODEIPVVAIMATGGIRAMTSLYQLAGLGLDCVYITGASGTWALANLY 180

181 EDPEWSQDLAGTELLKTQVTNKNLGVLAAPSOQRYOELABRLGVPSCFTNLWALI 240

181 EDPEWSQDLAGTELLKTQVTNKNLGVLAAPSOQRYOELABRLGVPSCFTNLWALI 240

241 NEALLHDEPHDKLSQREALSQGNPLPYCALNTKGSLTTFEFGWCEFPYEVGFP 300

241 NEALLHDEPHDKLSQREALSQGNPLPYCALNTKGSLTTFEFGWCEFPYEVGFP 300

301 KYGAFIPSELFSGEFFWQMLMKRLPESRICFLEGIWNSLYAANLQSLYWAESPQFWR 360

301 KYGAFIPSELFSGEFFWQMLMKRLPESRICFLEGIWNSLYAANLQSLYWAESPQFWR 360

361 WVRNQNANLDEQVPLKIEBPPSTAGRIAEFFDILLTWRLAQATHNFLRLGLHFKDYQ 420

361 WVRNQNANLDEQVPLKIEBPPSTAGRIAEFFDILLTWRLAQATHNFLRLGLHFKDYQ 420

QY 421 HPHFSTWKAATLTDGLPNQITPSEPHCLLDVGLINTSCLPLLOPTRDVLILSLDYNLH 480
Db 421 HPHFSTWKAATLTDGLPNQITPSEPHCLLDVGLINTSCLPLLOPTRDVLILSLDYNLH 480
QY 481 GAFQQLQLLGRFCQEQGIFPPISPSPEQLOPRECHTFSDPTCPGAPAVLHPSGVRRT 540
Db 481 GAFQQLQLLGRFCQEQGIFPPISPSPEQLOPRECHTFSDPTCPGAPAVLHPSGVRRT 540
QY 541 PEEAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYVNCNNQQLLEALRQAVRRR 600
Db 541 PEEAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYVNCNNQQLLEALRQAVRRR 600
QY 601 QRRPH 605
Db 601 QRRPH 605

RESULT 2

AAU10696
ID AAU10696 standard; protein; 778 AA.

XX AAU10696;

XX 25-FEB-2002 (first entry)

DT Human cPLA2-beta enzyme.

XX DE
XX KW Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta;
KW U937 cell; membrane phospholipid turnover; intracellular signalling;
KW arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis;
KW psoriasis; asthma; inflammatory bowel disease; antiinflammatory.

XX OS Homo sapiens.

XX US6287838-B1.

XX 11-SEP-2001.

XX 13-DEC-1999; 99US-00460145.

XX 24-JAN-1997; 97US-00788975.

XX (GENY) GENETICS INST INC.

XX Kriz R, Song C;

XX WPI: 2002-054342/07.

XX N-PSDB; AAS17362.

XX Novel cytosolic phospholipase A2-beta enzyme encoding polynucleotide,
PT useful for producing the enzyme for use in assays to discover enzyme
PT antagonists.

XX Claim 1; Col 15-19; 19pp; English.

XX The present invention relates to a novel calcium-independent cytosolic
XX phospholipase A2 (cPLA2)-beta enzyme and the cDNA sequence encoding it.
XX The cDNA clone is isolated from U937 cells. The cPLA2 enzyme is active in
XX membrane phospholipid turnover and in regulation of intracellular
XX signalling mediated by the arachidonic acid cascade. The invention
XX describes a method for producing phospholipase enzymes which can be used
XX to identify inhibitors of their function. The inhibitors can be used
XX to treat inflammatory disorders such as rheumatoid arthritis, psoriasis,
XX asthma, and inflammatory bowel disease. The present sequence represents
XX human cPLA2-beta enzyme

XX SQ Sequence 778 AA;

Query Match 85.5%; Score 2767.5; DB 5; Length 778;

Best Local Similarity 87.6%; Pred. No. 2.5e-248;

Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

QY 24 TGLVLVFCAPCPFFPFEMESLSVAQGVQWRDLGSLQPPPLGFRKFSCLSPSSWDYR 83

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184  TGTFRHCPA-C-----WQE-LSI-----RLQDAPEEQKAPLSALPSQVVR 225
84  -----LRELAVRLGFGPCAEQAFLSRRKQVVAALRQALQDGD 123
226  LVFPTSOEPLMRVELKKEAGLRELAVRLGFGPCAEQAFLSRRKQVVAALRQALQDGD 285
124  LOEDEIPVVAIMATGGIRAMTSYQQLAGLKGELGLDCVSYITGASGSTMALANLYEDP 183
286  LOEDEIPVVAIMATGGIRAMTSYQQLAGLKGELGLDCVSYITGASGSTMALANLYEDP 345
184  EWSQKDLAGTTELLKTQVTKNKLGVLPQSOLQRYQELAEARLGLHFKDYFOHPH 243
346  EWSQKDLAGTTELLKTQVTKNKLGVLPQSOLQRYQELAEARLGLHFKDYFOHPH 405
244  LLHDEPHDKLSDQREALSHGQNPPIYCALNTKGQSLTTFEFGWCEFSPEYVGFPPKYG 303
406  LLHDEPHDKLSDQREALSHGQNPPIYCALNTKGQSLTTFEFGWCEFSPEYVGFPPKYG 465
304  AFIPSELFSGSEFFMGQMLKRLPESRICFLEGIWNSLYAANLQDSLYWASEPSQFMDRWR 363
466  AFIPSELFSGSEFFMGQMLKRLPESRICFLEGIWNSLYAANLQDSLYWASEPSQFMDRWR 525
364  NOANLDKEQVPLLKIEEPPSTAGRIAEFTDLLTWRLAQATHNLRGLHFKDYFOHPH 423
526  NOANLDKEQVPLLKIEEPPSTAGRIAEFTDLLTWRLAQATHNLRGLHFKDYFOHPH 585
424  FSTWKATTLDLGNLQTPSEPHCLLDVGYLINTSCPLLPQTRDVLILSLDYNLHGAF 483
586  FSTWKATTLDLGNLQTPSEPHCLLDVGYLINTSCPLLPQTRDVLILSLDYNLHGAF 645
484  QQLQLLGRFCOEQIGIPPPISPSPEQLOPRECHTFSPTCPGAPAVLHF----- 533
646  QQLQLLGRFCOEQIGIPPPISPSPEQLOPRECHTFSPTCPGAPAVLHFPLVSDSFREY 705
534  -SSGVRTPEEAAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYVNCNQEQLLEAL 592
706  SAPGVRTPEEAAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYVNCNQEQLLEAL 765
593  ROAVRRRRQRPH 605
766  ROAVRRRRQRPH 778

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RESULT 3

ABG76482

ID ABG76482

XX AC ABG76482;

XX AC ABG76482;

XX DT 10-MAY-2003 (first entry)

XX DE Human partial cytosolic phospholipase A2-beta, cPLA2-beta.

XX DE Human; calcium independent cytosolic phospholipase A2-beta; cPLA2-beta;

XX KW antiinflammatory; arachidonic acid cascade; enzyme;

XX KW inflammatory condition.

XX OS Homo sapiens.

XX PN US6482625-B1.

XX PD 19-NOV-2002.

XX PF 29-JUN-2001; 2001US-00895547.

XX PR 24-JAN-1997; 97US-00788975.

XX PR 13-DEC-1999; 99US-00460145.

XX PA (GEM) GENETICS INST LLC.

XX PI Kriz R, Song C;

XX PI Kriz R, Song C;

WPI; 2003-287361/28.

N-PSDB; ABX11893.

XX Novel purified calcium-independent cytosolic phospholipase A2-beta

PT enzyme, useful for screening compounds having antiinflammatory activity

PT mediated by the arachidonic acid cascade.

XX Claim 2; Col 13-18; 19pp; English.

XX The invention relates to a purified phospholipase enzyme (calcium-

CC independent cytosolic phospholipase A2-beta enzyme) peptide appearing as

CC ABG76482 encoded by a polynucleotide appearing as ABX11893. The protein

CC has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoyl

CC -2- (1,4C)-arachidonyl- phosphatidylcholine. cPLA2-beta is useful for

CC assaying chemical agents for antiinflammatory activity mediated by the

CC various components of the arachidonic acid cascade. cPLA2-beta is also

CC useful in the development of polyclonal and monoclonal antibodies which

CC are useful as research or diagnostic tools, and to study phospholipase

CC A2 activity and inflammatory conditions. The present sequence represents

CC a partial cPLA2-beta protein

XX Sequence 778 AA;

SQ

Query Match

Best Local Similarity 85.5%; Score 2767.5; DB 6; Length 778;

Matches 537; Conservative 87.6%; Fred No. 2.5e-248; Mismatches 22; Indels 49; Gaps 6;

QY 24 TGLLVLPAPCPPTFFEMESLSVAQAGVQWRDLGSLQPPPLGFRKFSCLSLPSSWDYR 83

DB 184 TGTFRHCPA-C-----WQE-LSI-----RLQDAPEEQKAPLSALPSQVVR 225

QY 84 -----LRELAVRLGFGPCAEQAFLSRRKQVVAALRQALQDGD 123

DB 226 LVFPTSOEPLMRVELKKEAGLRELAVRLGFGPCAEQAFLSRRKQVVAALRQALQDGD 285

QY 124 LOEDEIPVVAIMATGGIRAMTSYQQLAGLKGELGLDCVSYITGASGSTMALANLYEDP 183

DB 286 LOEDEIPVVAIMATGGIRAMTSYQQLAGLKGELGLDCVSYITGASGSTMALANLYEDP 345

QY 184 EWSQKDLAGTTELLKTQVTKNKLGVLPQSOLQRYQELAEARLGLHFKDYFOHPH 243

DB 346 EWSQKDLAGTTELLKTQVTKNKLGVLPQSOLQRYQELAEARLGLHFKDYFOHPH 405

QY 244 LLHDEPHDKLSDQREALSHGQNPPIYCALNTKGQSLTTFEFGWCEFSPEYVGFPPKYG 303

DB 406 LLHDEPHDKLSDQREALSHGQNPPIYCALNTKGQSLTTFEFGWCEFSPEYVGFPPKYG 465

QY 304 AFIPSELFSGSEFFMGQMLKRLPESRICFLEGIWNSLYAANLQDSLYWASEPSQFMDRWR 363

DB 466 AFIPSELFSGSEFFMGQMLKRLPESRICFLEGIWNSLYAANLQDSLYWASEPSQFMDRWR 525

QY 364 NOANLDKEQVPLLKIEEPPSTAGRIAEFTDLLTWRLAQATHNLRGLHFKDYFOHPH 423

DB 526 NOANLDKEQVPLLKIEEPPSTAGRIAEFTDLLTWRLAQATHNLRGLHFKDYFOHPH 585

QY 424 FSTWKATTLDLGNLQTPSEPHCLLDVGYLINTSCPLLPQTRDVLILSLDYNLHGAF 483

DB 586 FSTWKATTLDLGNLQTPSEPHCLLDVGYLINTSCPLLPQTRDVLILSLDYNLHGAF 645

QY 484 QQLQLLGRFCOEQIGIPPPISPSPEQLOPRECHTFSPTCPGAPAVLHF----- 533

DB 646 QQLQLLGRFCOEQIGIPPPISPSPEQLOPRECHTFSPTCPGAPAVLHFPLVSDSFREY 705

QY 534 -SSGVRTPEEAAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYVNCNQEQLLEAL 592

DB 706 SAPGVRTPEEAAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYVNCNQEQLLEAL 765

QY 593 ROAVRRRRQRPH 605

DB 766 ROAVRRRRQRPH 778

CC are useful as research or diagnostic tools, and to study phospholipase
 CC A2 activity and inflammatory conditions. The present sequence represents
 CC the cPLA2-beta protein
 XX
 XX Sequence 797 AA;

Query Match 85.5%; Score 2767.5; DB 6; Length 797;
 Best Local Similarity 87.6%; Pred. No. 2.6e-248;
 Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;
 QY 24 TGLLVLCFPCAPCPFFFFFMESLSVAQGVQWRDLGSLQPPPLGFKFSCLSLPSWDYR 83
 Db 203 TGTFRFHCPA-C-----WQEQ-LSI-----RLQDAPEEQKAPLSALPGQVVR 244
 QY 84 -----LRELAVALRGFGPCAEQAFSLRRKQVVAALRQALQDGD 123
 Db 245 LVFPTSQBLMRVELKKEAGRELAVRLGFGCAEQAFSLRRKQVVAALRQALQDGD 304
 QY 124 LQDEIPVVAIMATGGIRAMTSLYGQLAGLKGELGLDCVSYITGASGSTWALANLYEDP 183
 Db 305 LQDEIPVVAIMATGGIRAMTSLYGQLAGLKGELGLDCVSYITGASGSTWALANLYEDP 364
 QY 184 EWSQDLAGPTTELLKTQVTKNKLGVLAQSLQRYQELAEARLGYPCFTNLWALINEA 243
 Db 365 EWSQDLAGPTTELLKTQVTKNKLGVLAQSLQRYQELAEARLGYPCFTNLWALINEA 424
 QY 244 LLHDEPHDKLSQREALSHGQNPLPIYCALNTKQSLTTTFEGWCEFSFVEVGFPGYK 303
 Db 425 LLHDEPHDKLSQREALSHGQNPLPIYCALNTKQSLTTTFEGWCEFSFVEVGFPGYK 484
 QY 304 AFIPSELFGSEFFMGQIMKRLPESRICFLEGIWNSLYAANLQDSLYWASEPQFWRWVR 363
 Db 485 AFIPSELFGSEFFMGQIMKRLPESRICFLEGIWNSLYAANLQDSLYWASEPQFWRWVR 544
 QY 364 NQANLDEQVPLLKIEEPPSTAGRIAEFFTDLLTWRLAQATHNLRGLHFKDYFQHPH 423
 Db 545 NQANLDEQVPLLKIEEPPSTAGRIAEFFTDLLTWRLAQATHNLRGLHFKDYFQHPH 604
 QY 424 FSTWKATTLGPNLQTPSEPHCLLDVGYLINTSCPLLPQTRDVLILSLDYNLHGAF 483
 Db 605 FSTWKATTLGPNLQTPSEPHCLLDVGYLINTSCPLLPQTRDVLILSLDYNLHGAF 664
 QY 484 QQLQLGRFCQEQGIPFPPIPSPEEQLOPRECHTFSDPTCPGAPAVLHF-----533
 Db 665 QQLQLGRFCQEQGIPFPPIPSPEEQLOPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 724
 QY 534 -SSGVRRTPEAAAGEVNLSSSDSPYHTKYTSQEDVDKLLHLTHYVNCNNOQLLEAL 592
 Db 725 SAPGVRRTPEAAAGEVNLSSSDSPYHTKYTSQEDVDKLLHLTHYVNCNNOQLLEAL 784
 QY 593 RQAVQRRQRPRH 605
 Db 785 RQAVQRRQRPRH 797

RESULT 6
 AA51557
 ID AA51557 standard; protein; 913 AA.
 XX
 AC
 XX
 XX
 DT 18-MAY-2000 (first entry)
 XX
 DE Human PLA2 protein.
 XX
 KW PLA2; phospholipase A2; phosphatide 2-acyl hydrolase; human; therapy;
 XX arachidonic acid; lysophospholipid; Alzheimer's disease.
 OS Homo sapiens.
 XX
 PN US6025178-A.
 XX
 PD 15 FEB 2000.

XX 28-MAR-1997; 97US-00827208.
 XX 29-MAR-1996; 96US-0014608P.
 XX (ELIL) LILLY & CO ELI.
 XX Sharp JD, Striffler BA, Chou XC, Kramer RM, Pickard RT;
 DR WPI; 2000-181816/16.
 XX N-PSDB; AA288756, AA288757.
 XX An isolated amino acid having phospholipase (PL)A2 activity is useful in
 PT assays to identify inhibitors having a therapeutic benefit, such as
 PT inhibiting the central role of PLA2 in the inflammatory component of
 PT Alzheimer's disease.
 XX Claim 1; Col 53-58; 32pp; English.
 PS This invention describes a novel human phospholipase A2 (PLA2) protein
 CC (I) and its encoding nucleic acid. The amino acid (I) releases
 CC arachidonic acid in specific tissues characterized by unique membrane
 CC phospholipids, by generating lysophospholipid species which are
 CC deleterious to membrane integrity or by remodeling of unsaturated species
 CC of membrane phospholipids through deacylation/reacylation mechanisms. The
 CC amino acid is useful in assays to identify inhibitors having a
 CC therapeutic benefit, such as inhibiting the central role of PLA2 in the
 CC inflammatory component of Alzheimer's disease. The amino acid (I) allows
 CC sensitive and rapid screening and identification of inhibitors of
 CC phospholipase A2. This sequence represents the human PLA2 protein (also
 CC known as phosphatide 2-acyl hydrolase)
 XX
 SQ Sequence 913 AA;

Query Match 85.5%; Score 2767.5; DB 3; Length 913;
 Best Local Similarity 87.6%; Pred. No. 3.2e-248;
 Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;
 QY 24 TGLLVLCFPCAPCPFFFFFMESLSVAQGVQWRDLGSLQPPPLGFKFSCLSLPSWDYR 83
 Db 319 TGTFRFHCPA-C-----WQEQ-LSI-----RLQDAPEEQKAPLSALPGQVVR 360
 QY 84 -----LRELAVALRGFGPCAEQAFSLRRKQVVAALRQALQDGD 123
 Db 361 LVFPTSQBLMRVELKKEAGRELAVRLGFGCAEQAFSLRRKQVVAALRQALQDGD 420
 QY 124 LQDEIPVVAIMATGGIRAMTSLYGQLAGLKGELGLDCVSYITGASGSTWALANLYEDP 183
 Db 421 LQDEIPVVAIMATGGIRAMTSLYGQLAGLKGELGLDCVSYITGASGSTWALANLYEDP 480
 QY 184 EWSQDLAGPTTELLKTQVTKNKLGVLAQSLQRYQELAEARLGYPCFTNLWALINEA 243
 Db 481 EWSQDLAGPTTELLKTQVTKNKLGVLAQSLQRYQELAEARLGYPCFTNLWALINEA 540
 QY 244 LLHDEPHDKLSQREALSHGQNPLPIYCALNTKQSLTTTFEGWCEFSFVEVGFPGYK 303
 Db 541 LLHDEPHDKLSQREALSHGQNPLPIYCALNTKQSLTTTFEGWCEFSFVEVGFPGYK 600
 QY 304 AFIPSELFGSEFFMGQIMKRLPESRICFLEGIWNSLYAANLQDSLYWASEPQFWRWVR 363
 Db 601 AFIPSELFGSEFFMGQIMKRLPESRICFLEGIWNSLYAANLQDSLYWASEPQFWRWVR 660
 QY 364 NQANLDEQVPLLKIEEPPSTAGRIAEFFTDLLTWRLAQATHNLRGLHFKDYFQHPH 423
 Db 661 NQANLDEQVPLLKIEEPPSTAGRIAEFFTDLLTWRLAQATHNLRGLHFKDYFQHPH 720
 QY 424 FSTWKATTLGPNLQTPSEPHCLLDVGYLINTSCPLLPQTRDVLILSLDYNLHGAF 483
 Db 721 FSTWKATTLGPNLQTPSEPHCLLDVGYLINTSCPLLPQTRDVLILSLDYNLHGAF 780
 QY 484 QQLQLGRFCQEQGIPFPPIPSPEEQLOPRECHTFSDPTCPGAPAVLHF-----533
 Db 781 QQLQLGRFCQEQGIPFPPIPSPEEQLOPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 840

QY 534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYNVNNQOLLEAL 592
Db 841 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYNVNNQOLLEAL 900
QY 593 ROAVORRRORRPH 605
Db 901 ROAVORRRORRPH 913

RESULT 7
AAB74635
ID AAB74635 standard; protein; 913 AA.
AC AAB74635;
XX 23-MAY-2001 (first entry)
XX Phospholipase A2 (PLA2) protein sequence SEQ ID NO:3.
DE Phospholipase A2; PLA2; antiinflammatory; inflammatory condition;
KW rheumatoid arthritis; psoriasis; asthma; cytosolic PLA2; cPLA2.
XX Homo sapiens.
XX US6197569-B1.
XX 06-MAR-2001.
XX 07-FEB-2000; 2000US-00500358.
XX 29-MAR-1996; 96US-0014608P.
PR 19-MAR-1997; 97US-0041264P.
PR 28-MAR-1997; 97US-00827208.
XX (ELIL) LILLY & CO ELI.
XX Chou XC, Kramer RM, Pickard RT, Sharp JD, Striffler BA;
WPI; 2001-256372/26.
N-PSDB; AAF74998, AAF74999.
Novel nucleic acid molecules encoding phospholipase A2 enzyme, useful in
screening assays for identifying compounds that inhibit or block
phospholipase A2 enzyme activity.

Claim 1; Col 53-58; 32pp; English.
The present invention describes an isolated polynucleotide (I),
comprising a 3085 base pair phospholipase A2 (PLA2) sequence (given in
AAAF74999), encoding a 913 residue phospholipase A2 protein sequence
(given in AAB74635), or a nucleotide sequence which hybridises under
stringent conditions to the above mentioned nucleotide sequence. Also
described are: (1) an isolated polynucleotide (II) comprising an 8517
base pair sequence, given in AAF74998; (2) an expression vector (III)
comprising (I) and an expression control sequence; (3) a host cell
transformed with (III); (4) an expression vector (IV) comprising (II)
operably linked to an expression control sequence; and (5) a host cell
operably linked to an expression control sequence. The host cells
inhibit or block cytosolic PLA2 (cPLA2) enzyme activity. The host cells
transformed or transfected with cPLA2 enzymes in large
quantities which are useful in screening assays for discovering agents
that inhibit PLA2. The inhibitors identified are useful for treating
inflammatory conditions such as rheumatoid arthritis, psoriasis, or
asthma. (I) is also useful in the detection of mutant genomic DNA which
has been digested with restriction enzymes and run on an electrophoretic
gel by hybridising to the genomic DNA

Sequence 913 AA;
Query Match 85.5%; Score 2767.5; DB 4; Length 913;
Best Local Similarity 87.6%; Pred. No. 3.2e-248;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

QY 24 TGLLVLCBAPCPFFFFEMESLSVAQACQVQWRDLGSLQPPPLGPKFRFSCLSLPSSWDYR 83
Db 319 TGTFRFHCPA-C-----WEQE--LSI-----RLQDAPEEQKAPLSALPSCQVYR 360
QY 84 -----LRELAVRLGFGPCAEQAFLSRRKQVVAALRQALQDGD 123
Db 361 LVEFTSQEPIMRVELKKEAGRELAVRLGFGPCAEQAFLSRRKQVVAALRQALQDGD 420
QY 124 LOEDEIPVVAIMATGGGIRAMTSLYQLAGLKGELGLDCVSYITGASGWTWALANIYEDP 183
Db 421 LOEDEIPVVAIMATGGGIRAMTSLYQLAGLKGELGLDCVSYITGASGWTWALANIYEDP 480
QY 184 EMSQKDLAGPTTELLKTQVTNKNLGVLAQSLQRYQELAEARLGVPSCTNLWALINEA 243
Db 481 EMSQKDLAGPTTELLKTQVTNKNLGVLAQSLQRYQELAEARLGVPSCTNLWALINEA 540
QY 244 LHDEPHDKLSDOREALSHGQNPPLIYCALNTKGOSLTTFEGEWCEFSFYEVGFPKY 303
Db 541 LHDEPHDKLSDOREALSHGQNPPLIYCALNTKGOSLTTFEGEWCEFSFYEVGFPKY 600
QY 304 AFIPSELFGSEFFMGQMKRKLPSRICFLEGIWSNLYAANLQDSLYWASEPQFWDWRVR 363
Db 601 AFIPSELFGSEFFMGQMKRKLPSRICFLEGIWSNLYAANLQDSLYWASEPQFWDWRVR 660
QY 364 NQANLKEQVPLKIEBPPSTAGRIAEFFTDLLTWRLAQATHNLFGLHFKDYFOHPH 423
Db 661 NQANLKEQVPLKIEBPPSTAGRIAEFFTDLLTWRLAQATHNLFGLHFKDYFOHPH 720
QY 424 FSTWKATTLGDLNQLTPSEPHCLLDVGYLINTSCPLLPQTRDVLILSLDNLHGAF 483
Db 721 FSTWKATTLGDLNQLTPSEPHCLLDVGYLINTSCPLLPQTRDVLILSLDNLHGAF 780
QY 484 QQLQLGRFCQEQGIPFPPIPSPEEQLOPRECHTFSDPTCPGAPAVLHF----- 533
Db 781 QQLQLGRFCQEQGIPFPPIPSPEEQLOPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 840
QY 534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYNVNNQOLLEAL 592
Db 841 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYNVNNQOLLEAL 900
QY 593 ROAVORRRORRPH 605
Db 901 ROAVORRRORRPH 913
RESULT 8
AAB82415
ID AAB82415 standard; protein; 913 AA.
AC AAB82415;
XX 06-AUG-2001 (first entry)
DT Human phospholipase A2.
DE Phospholipase A2; PLA2; bPLA2; PLA2-beta; inhibitor; screening;
KW antiinflammatory; human; Alzheimer's disease; therapy.
XX Homo sapiens.
XX US6242206-B1.
XX 05-JUN-2001.
XX 07-FEB-2000; 2000US-00498809.
XX 29-MAR-1996; 96US-0014608P.
PR 19-MAR-1997; 97US-0041264P.
PR 28-MAR-1997; 97US-00827208.
XX (ELIL) LILLY & CO ELI.
XX

PI Chou X, Kramer RM, Pickard RT, Sharp JD, Striffler BA;
XX
WPI: 2001-366537/38.
DR N-ESDB; AAF90487, AAF90488.
DR

PT Assays to evaluate the effectiveness of inhibitors of phospholipase A2,
PT used to screen candidate compounds, comprise recombinant expression of a
PT novel phospholipase A2.

PS Claim 1(a); Col 53-58; 32pp; English.

The present sequence is that of a novel human phospholipase A2 (PLA2, also referred to bPLA2 or PLA2-beta). PLA2 liberates arachidonic acid from phospholipids, leading to the production of eicosanoids involved in inflammatory reaction. A claimed assay for evaluating the effectiveness of a compound as an inhibitor of PLA2 involves culturing a cell transformed with an expression vector comprising PLA2 genomic DNA or cDNA (see AAF90487-98), isolating the PLA2, contacting it with a candidate compound, and determining whether the PLA2 activity has been inhibited. The assay provides rapid and efficient screening for new antiinflammatory drugs that inhibit the arachidonic acid cascade. These may be especially useful in the treatment of the inflammatory component of Alzheimer's disease

Sequence 913 AA;

Query Match 85.5%; Score 2767.5; DB 4; Length 913;
Best Local Similarity 87.6%; Pred. No. 3.2e-248;
Matches 537; Conservative 5; Mismatched 22; Indel 1

Qy 24 TGLVLFCAPCPFFFEFMESSLVAQGVOWRDLGSLQPPLGFKFSCLSLSSWDYR 83
 ||| :||| | : :|||
Db 319 TGTRFHCPA-C-----WEQE-LSI-----RLQDAPEQLKAPUSALPSGGVQR 360

Qy 84 -----LRLAVRIGFGPCAEQAFLSRRKQTVAALRQLQLDGD 123
 |||||
Dδ 361 LVFPTSQEPLMRVELKEAGIRELAVRIGFGPCAEQAFLSRRKQTVAALRQLQLDGD 420

QY 124 LQDEIPVVAIMATGGIRAMTSIYQLAGIKELGLLDCVSYITGSGSTWALANLYEDP 183
|||||
Db 421 LQDEIPVVAIMATGGIRAMTSIYQLAGIKELGLLDCVSYITGSGSTWALANLYEDP 480

Qy

184 EWSKDLAGTELTQTQVTKNKLGVLPASQLQRQELAERALGYSCCTNIWALINEA 243
|||||
|||||

Dd

481 EWSKDLAGTELTQTQVTKNKLGVLPASQLQRQELAERALGYSCCTNIWALINEA 540

244 LLDPEPHDKLSQREALSHGQNPLPTICALNTKGSLTTFEGWCEFSFYEVGFPKYG 303
|||||
541 LLDPEPHDKLSQREALSHGQNPLPTICALNTKGSLTTFEGWCEFSFYEVGFPKYG 600
|||||

304 AFIPSELFSGSEFMGQMKRLPESRICFLEGIWSNLYAANQDSLYWASEPSPQFDRWVR 363
 |||||
 601 AFIPSELFSGSEFMGQMKRLPESRICFLEGIWSNLYAANQDSLYWASEPSPQFDRWVR 660
 |||||

364 QY NQANLDKEQVPLKIEEPSTAGRAEFTDLLTWRLAQATNFIURLGHLFHFKDYQHPH 423
 |||||
 661 Db NQANLDKEQVPLKIEEPSTAGRAEFTDLLTWRLAQATNFIURLGHLFHFKDYQHPH 720

424 PSTWKTATLDGLPNQITPSEPHCLLDVGYLINTSCPLPQTPRDVDLLSLDYNLHGAF 483
 721 PSTWKTATLDGLPNQITPSEPHCLLDVGYLINTSCPLPQTPRDVDLLSLDYNLHGAF 780

DY
Db

484 QQLQLGRFCQDGGIFPPISPSPEQLQPRECHTFSDPTCGAPAVLHF----- 533
|||||
781 QQLQLGRFCQDGGIFPPISPSPEQLQPRECHTFSDPTCGAPAVLHFFLVDSDFREY 840
|||||

534 -SSGVRTPFEAAAGEVNLSSDSPHYHTKVTSQEDVDKLIHLTHYVNCNQEQLLEAL 592
:
841 SAPGVRTPFEAAAGEVNLSSDSPHYHTKVTSQEDVDKLIHLTHYVNCNQEQLLEAL 900

593 RQAVQRRFQRRPH 605
|||||
901 RQAVQRRFQRRPH 913

RESULT 9	
AAB21140	
ID	AAB21140 standard; protein; 533 AA.
XX	
AC	
XX	AAB21140;
XX	
DT	19-JAN-2001 (first entry)
XX	
DE	Human cytosolic phospholipase A2 cPLA2 beta.

XX	
KW	Human; cytosolic phospholipase A2 beta; cPLA
KW	inflammatory disease; crystal structure.
XX	

OS Homo sapiens.
XX
PN WO200047763-A1.

XX
PD
17-AUG-2000.
XX
XX

FF 14-FEB-2000; 2000WO-US003745.
XX
PR 15-FEB-1999; 99US-00250083.
XX

PA (GEMY) GENETICS INST INC.
XX
PI Dessan A, Somers WS. Stahl MI. Seehra JS.

XX
DR WPI; 2000-558219/51.
XX

PT New crystalline cytosolic phospholipase A2 (cPLA2) is a species which is an agonist or antagonist of that can be used to prevent or treat inflammatory conditions.

XX
PS Disclosure; Fig 4; 71pp; English.
XX

The present sequence is the human cytosolic protein. The invention concerns the elucidation of the protein and its use in drug design. The

CC identify treatments for inflammation-related
CC rheumatoid arthritis, psoriasis, asthma, infl
CC diseases such as osteoporosis, colitis, myelo
CC wasting and rheumatoid arthritis

XX
XX
SQ

Query Match 85.5%; Score 2765.5; D
Best Local Similarity 97.6%; Pred. No. 2.1e-2
Matches 520; Conservative 1; Mismatches

84 LRELAVRLGFGPCAEQAFLSRRQVVAAALRQALQ

144 MTSLYGQLAGLKEGLDCVSYITGASGSTWALNL

bb 61 MTSLYGQLAGLKEIGLLDCVSYITGASGSTWALNL

204 NKLGVLPASQLQRYRQELAEARLGYPSCFETNLWAL

bb
121 NKLGVLAPSQLQRYRQELAEARLGYPSCTNLWL
264

204 GQNPLPIYCALNTKGQSLTTTFEGGEWCEFSPIYEVGFT
181 GQNPLPIYCALNTKGQSLTTTFEGGEWCEFSPIYEVGFT

324 LPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDDE
|||
241 LPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDDE

384 TAGRIAEFFDILLTRPLAQAATHNFLRGLHFKDYFC

CC	electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 1020 AA;	
	Query Match 83.5%; Score 2700; DB 4; Length 1020;	
	Best Local Similarity 86.4%; Pred. No. 7.5e-242;	
	Matches 532; Conservative 5; Mismatches 27; Indels 52; Gaps 9;	
QY	24 TGLLVLCFCAPCPFFPPFFPPFEMESLSVAQAGVQWRDGLSGSLQPPPLGFKRFRFCLSPSSWDYR 83	
Db	423 TGTFRHCPA-C-----WEQE-LSI-----RLQDAPEQKAPLSALPSGVVR 464	
QY	84 -----LRELAIVLGFPCAEQAFLSRRKQVVAAALRALQALDGD 123	
Db	465 LVFPTSQEPLMRVELKKEAGLRELAIVLGFPCAEQAFLSRRKQVVAAALRALQALDGD 524	
QY	124 LOEDEIPVVAIMATGGIRAMTSLYGQLAGLKEGLLDCVSYITGASGWTWALANLYEDP 183	
Db	525 LQDEIPVVAIMATGGIRAMTSLYGQLAGLKEGLLDCVSYITGASGWTWALANLYEDP 584	
QY	184 EMSQKDLAGTELLKTQVTKNKLGVLAPOQRYRQELAEARLGYSCFTNLWALINEA 243	
Db	585 EMSQKDLAGTELLKTQVTKNKLGVLAPOQRYRQELAEARLGYSCFTNLWALINEA 644	
QY	244 LLHDEPHDKLSDOREALSHQONPLPIYCALNTKGQSLTTFEGCEWCFSPYEVGFPPKYG 303	
Db	645 LLHDEPHDKLSDOREALSHQONPLPIYCALNTKGQSLTTFEGCEWCFSPYEVGFPPKYG 704	
QY	304 AFIPSELFSGSEFFFMQMLKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRAWV- 362	
Db	705 AFIPSELFSGSEFFFMQMLKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRAWV 764	
QY	363 RNQANLDEKQVPLLKIEEPPSTAGRIAEFFTDLLTWRLAQATHFLRGLH-FHKDYFOH 421	
Db	765 RNQANLDEKQVPLLKIEEPPSTAGRIAEFFTDLLTWRLAQATHFLRGLRIFHKDYFOH 824	
QY	422 PHFSTWKATTLDDGLPNQLTPSEPHCLLDVGY-LINTSCLPLLOTPRDVDLILSDYNLH 480	
Db	825 PHFSTWKATTLDDGLPNQLTPSEPHCLLDGGYTLINTSCLPLLOTPRDVDLILSDYNLH 884	
QY	481 GAFQOLQLLGRFCOEGIPFPPIPSPEQLOPRECHTFSPTCPGAPAVLHF----- 533	
Db	885 GAFQOLQLLGRFCOEGIPFPPIPSPEQLOPRECHTFSPTCPGAPAVLHFPLVSDSF 944	
QY	534 ----SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYNNCNOBOLL 589	
Db	945 REYSAPGVRRTPPEEAAAGEVNLSSSDSPYHYTKVTSQEDVDKLLHLTHYNNCNOBOLL 1004	
QY	590 EALROAVQRRRRRPH 605	
Db	1005 EALROAVQRRRRRPH 1020	
RESULT 11		
ABG20154		
ID	ABG20154 standard; protein; 1040 AA.	
XX		
AC	ABG20154;	
XX		
DT	18-FEB-2002 (first entry)	
XX		
DE	Novel human diagnostic protein #20145.	
XX		
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;	
KW	food supplement; medical imaging; diagnostic; genetic disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200175067-A2.	
XX		
PD	11-OCT-2001.	
XX		

Db	301 TAGRIAEFTDILLTWRLPQAATHNLFGLHFKDFQHFHFTWKATTLDDGLPNQLTPSE 360	
QY	444 PHLCLLDVGYLINTSCLPLLOTPRDVDLILSDYNLHGAFQOLQLLGRFCOEGIPFPPI 503	
Db	361 PHLCLLDVGYLINTSCLPLLOTPRDVDLILSDYNLHGAFQOLQLLGRFCOEGIPFPPI 420	
QY	504 SPSPEQLOPRECHTFSPTCPGAPAVLHF-----SSGVRRTPEEAAAGEVNLSS 552	
Db	421 SPSPEQLOPRECHTFSPTCPGAPAVLHF-----SSGVRRTPEEAAAGEVNLSS 480	
QY	553 SSDSPHYTKVTSQEDVDKLLHLTHYNNCNOBOLLLEALRQAVQRRRRRPH 605	
Db	481 SSDSPHYTKVTSQEDVDKLLHLTHYNNCNOBOLLLEALRQAVQRRRRRPH 533	
RESULT 10		
ABG05871		
ID	ABG05871 standard; protein; 1020 AA.	
XX		
AC	ABG05871;	
XX		
DT	13-FEB-2002 (first entry)	
XX		
DE	Novel human diagnostic protein #5862.	
XX		
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;	
KW	food supplement; medical imaging; diagnostic; genetic disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200175067-A2.	
XX		
PD	11-OCT-2001.	
XX		
PF	30-MAR-2001; 2001WO-US008631.	
XX		
PR	31-MAR-2000; 2000US-00540217.	
PR	23-AUG-2000; 2000US-00649167.	
XX	(HYSE-) HYSEQ INC.	
PA	Dmanac RT, Liu C, Tang YT;	
PI		
XX	WPI; 2001-639362/73.	
DR	N-PSDB; AAS70058.	
XX		
XX	New isolated polynucleotide and encoded polypeptides, useful in	
PT	diagnostics, forensics, gene mapping, identification of mutations	
PT	responsible for genetic disorders or other traits and to assess	
PT	biodiversity.	
XX		
PS	Claim 20; SEQ ID NO 36230; 103pp; English.	
XX		
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II)	
CC	sequences. (I) is useful as hybridisation probes, polymerase chain	
CC	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,	
CC	and in recombinant production of (II). The polynucleotides are also used	
CC	in diagnostics as expressed sequence tags for identifying expressed	
CC	genes. (I) is useful in gene therapy techniques to restore normal	
CC	activity of (II) or to treat disease states involving (II). (II) is	
CC	useful for generating antibodies against it, detecting or quantitating a	
CC	polypeptide in tissue, as molecular weight markers and as a food	
CC	supplement. (II) and its binding partners are useful in medical imaging	
CC	of sites expressing (II). (I) and (II) are useful for treating disorders	
CC	involving aberrant protein expression or biological activity. The	
CC	polypeptide and polynucleotide sequences have applications in	
CC	diagnostics, forensics, gene mapping, identification of mutations	
CC	responsible for genetic disorders or other traits to assess biodiversity	
CC	and to produce other types of data and products dependent on DNA and	
CC	amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic	
CC	amino acid sequences of the invention. Note: The sequence data for this	
CC	patent did not appear in the printed specification, but was obtained in	

30-MAR-2001; 2001WO-US008631.
31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
(HYSE-) HYSBQ INC.
Drmanac RT, Liu C, Tang YT;
WPI; 2001-639362/73.
N-PSDB; AAS84341.
New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity.
Claim 20; SEQ ID NO 50513; 103pp; English.
The invention relates to isolated polynucleotide (I) and polypeptide (II)
sequences. (I) is useful as hybridisation probes, polymerase chain
reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polynucleotides are also used
in diagnostics as expressed sequence tags for identifying expressed
genes. (I) is useful in gene therapy techniques to restore normal
activity of (II) or to treat disease states involving (II). (II) is
useful for generating antibodies against it, detecting or quantitating a
polypeptide in tissue, as molecular weight markers and as a food
supplement. (II) and its binding partners are useful in medical imaging
of sites expressing (II). (I) and (II) are useful for treating disorders
involving aberrant protein expression or biological activities. The
polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
amino acid sequences of the invention. Note: The sequence data for this
patent did not appear in the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 1040 AA;
Query Match 80.7%; Score 2610.5; DB 4; Length 1040;
Best Local Similarity 84.3%; Pred. No. 1.7e-233;
Matches 520; Conservative 7; Mismatches 35; Indels 55; Gaps 11;
24 TGLLVLCPCAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKPSCLSLPSWDYR 83
430 TGTFRHCPA-C-----WEQE-LSI-----RLQDAPEQLKAPLSALPSGVVR 471
84 -----LRELAVRLGFGPCAEQAFLSRRKQVVAAALRQALQDGD 123
472 LVFPTSQELPMRVKELKEAGLRELAVRLGFGPCAEQAFLSRRKQVVAAALRQALQDGD 531
124 LQDEIPVVAIMATGGIRAMTSLYGQAGLKEGLLDVCVSYITGASGTWALANLYEDP 183
532 LQDEIPVVAIMATGGIRAMTSLYGQAGLKEGLLDVCVSYITGASGTWALANLYEDP 591
184 EWSQKDLAGTTELLKTQVTNKNKLGVLAPSOLQRYQELAEARLGYPCSTNWLALINEA 243
592 EWSQKDLAGTTELLKTQVTNKNKLGVLAPSOLQRYQELAEARLGYPCSTNWLALINEA 651
244 LLHDEPHDKLSQREALSQGNPLPYCYALNTKGSLTTFEGMCEFPSPYVGRPKYG 303
652 LLHDEPHDKLSQREALSQGNPLPYCYALNTKGSLTTFEGMCEFPSPYVGRPKYG 711
304 APTSELFGSEFFMGQMLKGLPSRICTFEGINSWLYAANLQSLYASPPQFWRWV- 362
712 APTSELFGSEFFMGQMLKGLPSRICTFEGINSWLYAANLQSLYASPPQFWRWVS 771
363 RNQANLDKEQVPLKTEEPSTAGRIAEFTDLLTWRLAQATQNFRLGRSIFHKDYFOH 421
|||||

Db 772 RNQANLDKEQVPLKTEEPSTAGRIAEFTDLLTWRLAQATQNFRLGRSIFHKDYFOH 831
Qy 422 PHESTWKATTDGLPNQLTPSEPHLCLLDVGY-LINTSCLPLOPTEDVDLLIISLDYNLH 480
Db 832 PHESTWKATTDGLPNQLTPSEPHLCLLDGGYTLINTSCLPLOPTEDVDLLIISLDYNLH 891
Qy 481 GAFQOQLLGRFCQEQGIFPPPIPSPEBQLOP-RECHTFSDFTCGAPAVLHF----- 533
Db 892 GAFQOQLLGRFCQEQGIFPPPIPSPEBQLOPWRSGHTFSDPTCFGAPAVLHFPLVSDS 951
Qy 534 -----SSGVRRTPEAAAGEVNLSSDSPHYTKVTSQEDVDKLLHLTHYNNVQNEQL 588
Db 952 FREYSAPGVRRTPEAAAGEVNLSSDSPHYTKVTSQEDVDKLLHLTHYNNVQNEQL 1011
Qy 589 LEAL--RQAVQRRQR 603
Db 1012 LGRLCAPGSGANGRRQRK 1028
RESULT 12
AAW75132
ID AAW75132 standard; protein; 483 AA.
XX
AC AAW75132;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1999 (first entry)
XX
DE Human secreted protein encoded by gene 11 clone HCENJ40.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
developmental abnormality; foetal deficiency; blood; allergy; renal;
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflammation; ischaemic shock; Alzheimer's disease; testenosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 29
FT Misc-difference /label= unknown
FT Misc-difference 483
FT Misc-difference /label= unknown
XX
FN WO9839446-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US004482.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 11-APR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;

PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;

PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;

PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;

XX WPI; 1998-609887/51.

DR N-PSDB; AAV34229.

XX PT New isolated human genes and the secreted polypeptides they encode -

PT useful for diagnosis and treatment of e.g. cancers, neurological

PT disorders, immune diseases, inflammation or blood disorders.

XX PS Claim 1; Page 326-327; 447pp; English.

XX CC This sequence represents a secreted human protein encoded by the gene

CC clone detailed in the descriptor line. The gene can be used to generate

CC fusion proteins by linking to the gene to a human immunoglobulin Fc

CC portion (e.g. AAV34145) for increasing the stability of the fused protein

CC as compared to the human protein only. The invention relates to 70 novel

CC genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino

CC acid sequences AAW75057-W75179) which are useful for preventing, treating

CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,

CC pathological conditions can be diagnosed by determining the amount of the

CC new polypeptides in a sample or by determining the presence of mutations

CC in the new polynucleotides. Specific uses are described for each of the

CC 70 polynucleotides, based on which tissues they are most highly expressed

CC in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct

CC PF field.) (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 483 AA;

Query Match 77.6%; Score 2509.5; DB 2; Length 483;

Best Local Similarity 96.9%; Pred. No. 1.3e-224;

Matches 467; Conservative 2; Mismatches 2; Indels 11; Gaps 1;

QY 135 MATGGIRAMTSLYGQLAGLGLDCVSYTGASGSTMALANIYEDPWSOKDLAFT 194

Db 1 MATGGIRAMTSLYGQLAGLGLDCVSYTGASGSTMALANIYEDPWSOKDLAFT 60

QY 195 ELLKTQVTKNKLGVLAQSLQRYQELAEARLGYPSCTNLWALINEALLHDEPHDKL 254

Db 61 ELLKTQVTKNKLGVLAQSLQRYQELAEARLGYPSCTNLWALINEALLHDEPHDKL 120

QY 255 SDQREALSHGQNPLPIYCALNTKGSLTTFEGWCEFSPEYVGPKYGAFIPSELFGSE 314

Db 121 SDQREALSHGQNPLPIYCALNTKGSLTTFEGWCEFSPEYVGPKYGAFIPSELFGSE 180

QY 315 FPMQIMXKRLPESRICFLEGIWSNLIYAANLQDSLYWASEPSQFWDWRVNOANLKEQVP 374

Db 181 FPMQIMXKRLPESRICFLEGIWSNLIYAANLQDSLYWASEPSQFWDWRVNOANLKEQVP 240

QY 375 ILKIEPPSTAGRIAEFFDILLTWPLAQATNHLGLHFHKDYFOHPHFSTWKATLDG 434

Db 241 ILKIEPPSTAGRIAEFFDILLTWPLAQATNHLGLHFHKDYFOHPHFSTWKATLDG 300

QY 435 LPNQLTPSEPPLCLLDVGYLINTSCLPLQPTRDVDLILSLDYNLHGAFOQLQLGRFCQ 494

Db 301 LPNQLTPSEPPLCLLDVGYLINTSCLPLQPTRDVDLILSLDYNLHGAFOQLQLGRFCQ 360

QY 495 EQGIPPPISPPEEQLOPRECHTFSDPTCPGAPAVLHPLFSDSPREVSAPGVRTPEE 543

Db 361 EQGIPPPISPPEEQLOPRECHTFSDPTCPGAPAVLHPLFSDSPREVSAPGVRTPEE 420

QY 544 AAAGEVNLSSDSPYHYTKVTSQEDVDKLLHLTHYVNCNNQQLLEALQAVQRQR 603

Db 421 AAAGEVNLSSDSPYHYTKVTSQEDVDKLLHLTHYVNCNNQQLLEALQAVQRQR 480

QY 604 PH 605

Db 481 PH 482

RESULT 13
AAW75067
ID AAW75067 standard; protein; 483 AA.
XX AC AAW75067;
XX DT 25-MAR-2003 (revised)
DT 28-JAN-1999 (first entry)
XX Human secreted protein encoded by gene 11 clone HCENJ40.
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
PH Misc-difference 29 /label= unknown
FT Misc-difference 483
FT Misc-difference 483 /label= unknown
XX
XX W09839446-A2.
XX PD 11-SEP-1998.
XX PF 06-MAR-1998; 98WO-US004482.
XX PR 07-MAR-1997; 97US-0038621P.
XX PR 07-MAR-1997; 97US-0040161P.
XX PR 07-MAR-1997; 97US-0040162P.
XX PR 07-MAR-1997; 97US-0040163P.
XX PR 07-MAR-1997; 97US-0040333P.
XX PR 07-MAR-1997; 97US-0040334P.
XX PR 07-MAR-1997; 97US-0040336P.
XX PR 11-APR-1997; 97US-0040626P.
XX PR 11-APR-1997; 97US-0043311P.
XX PR 11-APR-1997; 97US-0043312P.
XX PR 11-APR-1997; 97US-0043313P.
XX PR 11-APR-1997; 97US-0043314P.
XX PR 11-APR-1997; 97US-0043315P.
XX PR 11-APR-1997; 97US-0043588P.
XX PR 11-APR-1997; 97US-0043589P.
XX PR 11-APR-1997; 97US-0043576P.
XX PR 11-APR-1997; 97US-0043578P.
XX PR 11-APR-1997; 97US-0043580P.
XX PR 11-APR-1997; 97US-0043669P.
XX PR 11-APR-1997; 97US-0043670P.
XX PR 11-APR-1997; 97US-0043671P.
XX PR 11-APR-1997; 97US-0043672P.
XX PR 11-APR-1997; 97US-0043674P.
XX PR 23-MAY-1997; 97US-0047492P.
XX PR 23-MAY-1997; 97US-0047500P.
XX PR 23-MAY-1997; 97US-0047501P.
XX PR 23-MAY-1997; 97US-0047502P.
XX PR 23-MAY-1997; 97US-0047503P.
XX PR 23-MAY-1997; 97US-0047581P.
XX PR 23-MAY-1997; 97US-0047582P.
XX PR 23-MAY-1997; 97US-0047583P.
XX PR 23-MAY-1997; 97US-0047584P.
XX PR 23-MAY-1997; 97US-0047585P.
XX PR 23-MAY-1997; 97US-0047586P.
XX PR 23-MAY-1997; 97US-0047587P.
XX PR 23-MAY-1997; 97US-0047588P.
XX PR 23-MAY-1997; 97US-0047589P.

PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057761P.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JW;
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
WPI; 1998-609887/51.
N-PSDB; AAV34164.

New isolated human genes and the secreted polypeptides they encode -
useful for diagnosis and treatment of e.g. cancers, neurological
disorders, immune diseases, inflammation or blood disorders.

Claim 1; Page 285-287; 447pp; English.

CC This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAV34145) for increasing the stability of the fused protein
CC as compared to the human protein only. The invention relates to 70 novel
CC genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino
CC acid sequences AAV75057-W75179) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 70 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 483 AA;

Query Match 77.6%; Score 2509.5; DB 2; Length 483;
Best Local Similarity 96.9%; Pred. No. 1.3e-224;
Matches 467; Conservative 2; Mismatches 2; Indels 11; Gaps 1;
QY 135 MATGGIRAMTSYGLQAGLKLGLDVCVYITGASGWTALANLYDEPWSQKDLAAPT 194
Db 1 MATGGIRAMTSYGLQAGLKLGLDVCVYITGASGWTALANLYDEPWSQKDLAAPT 60
QY 195 ELLKTQTKNKLGLVAPSOLQRYQELARLGVSCFTNLWALINEALLHDEPHDKL 254
Db 61 ELLKTQTKNKLGLVAPSOLQRYQELARLGVSCFTNLWALINEALLHDEPHDKL 120
QY 255 SDQREALSHGONPLPIYCALNTKGSLTTFEFGWCEPSPYEVGPKYGAFIGPSELFGSE 314
Db 121 SDQREALSHGONPLPIYCALNTKGSLTTFEFGWCEPSPYEVGPKYGAFIGPSELFGSE 180
QY 315 PFMGQMKRLPESRICFLEGWNSNLYANLQDSLYWASEPQFWDWRVNRQANLDKEQVP 374
Db 181 PFMGQMKRLPESRICFLEGWNSNLYANLQDSLYWASEPQFWDWRVNRQANLDKEQVP 240
QY 375 LKKEBPSTAGRIAEFTDILLTWPLAQATHNLRGLHFKDYFOHPHFSTWKATLLDG 434
Db 241 LKKEBPSTAGRIAEFTDILLTWPLAQATHNLRGLHFKDYFOHPHFSTWKATLLDG 300
QY 435 LPNQLTPSEPHCLLDVGLINTSCLPLQPTRDVDLILSLDYNLHGAFQQLIGRFCC 494
Db 301 LPNQLTPSEPHCLLDVGLINTSCLPLQPTRDVDLILSLDYNLHGAFQQLIGRFCC 360
QY 495 EQGIFPPPIPSPEQLQPRECHTSDPTCPGAPAVLHP-----SSGVRTPEE 543
Db 361 EQGIFPPPIPSPEQLQPRECHTSDPTCPGAPAVLHP-----SSGVRTPEE 420
QY 544 AAAGEVNLSSDSPHYTKVTSOEDVDKLLHLTHVNCNBOLEALRQAVRRQR 603
Db 421 AAAGEVNLSSDSPHYTKVTSOEDVDKLLHLTHVNCNBOLEALRQAVRRQR 480
QY 604 PH 605
Db 481 PH 482

RESULT 14
AB001943
ID AB001943 standard; protein; 483 AA.
XX
XX AB001943;
AC
XX
DT 12-AUG-2003 (first entry)
XX
DE Novel human secreted protein #11.
XX
XX Human; immunoglobulin G; IgG; fragment of crystallisation; Fc;
XX immune system disorder; haematopoietic cell disorder;
KW immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
KW Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
KW blood coagulation disorder; blood platelet disorder; autoimmune disorder;

KW Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW glomerulonephritis; Grave's disease; allergic reaction;
KW graft-versus-host disease; hyperproliferative disorder; neoplasm;
KW infectious disease; nervous system disease; spinal cord disorder;
KW head trauma; stroke; tissue regeneration; congenital defect; trauma;
KW wound; burn; incision; ulcer; age disease; osteoporosis;
KW periodontal disease; liver failure; catabolism; anabolism; metabolism;
KW food additive; preservative; secreted protein.
XX
OS Homo sapiens.
XX
XX US2003027132-A1.
XX
XX 06-FEB-2003.
XX
XX 04-SEP-1998; 98US-00148545.
XX
XX 07-MAR-1997; 97US-0038621P.
XX 07-MAR-1997; 97US-0040161P.
XX 07-MAR-1997; 97US-0040162P.
XX 07-MAR-1997; 97US-0040163P.
XX 07-MAR-1997; 97US-0040333P.
XX 07-MAR-1997; 97US-0040334P.
XX 07-MAR-1997; 97US-0040336P.
XX 07-MAR-1997; 97US-0040626P.
XX 11-APR-1997; 97US-0043311P.
XX 11-APR-1997; 97US-0043312P.
XX 11-APR-1997; 97US-0043313P.
XX 11-APR-1997; 97US-0043314P.
XX 11-APR-1997; 97US-0043315P.
XX 11-APR-1997; 97US-0043568P.
XX 11-APR-1997; 97US-0043569P.
XX 11-APR-1997; 97US-0043576P.
XX 11-APR-1997; 97US-0043578P.
XX 11-APR-1997; 97US-0043580P.
XX 11-APR-1997; 97US-0043669P.
XX 11-APR-1997; 97US-0043670P.
XX 11-APR-1997; 97US-0043671P.
XX 11-APR-1997; 97US-0043672P.
XX 11-APR-1997; 97US-0043674P.
XX 23-MAY-1997; 97US-0047492P.
XX 23-MAY-1997; 97US-0047501P.
XX 23-MAY-1997; 97US-0047502P.
XX 23-MAY-1997; 97US-0047503P.
XX 23-MAY-1997; 97US-0047581P.
XX 23-MAY-1997; 97US-0047582P.
XX 23-MAY-1997; 97US-0047583P.
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PR 06-JUN-1997; 97US-0048964P.
 PR 06-JUN-1997; 97US-0048974P.
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 PR 22-AUG-1997; 97US-0056631P.
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 PR 22-AUG-1997; 97US-0056633P.
 PR 22-AUG-1997; 97US-0056636P.
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 PR 22-AUG-1997; 97US-0056874P.
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 PR 05-SEP-1997; 97US-0057761P.
 PR 06-MAR-1998; 98WO-US004482.
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 (ENDR// ENDRESS G A.
 (YUGG// YU G.
 (NIJJ// NI J.
 (FENG// FENG P.
 (YOUN// YOUNG P E.
 (GREE// GREENE J M.
 (FERE// FERRIE A M.
 (DUAN// DUAN R.
 (HUJJ// HU J.
 (FLOJ// FLORENCE K A.
 (OLSE// OLSEN H S.
 (EBNE// EBNER R.
 (BREW// BREWER L A.
 (SHIY// SHI Y.

Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
 Bednariik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
 Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 Shi Y;

WPI; 2003-466138/44.
 N-PSDB; AC008035.

Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing
 or treating deficiencies or disorders of the immune system, autoimmune
 disorders, hyperproliferative disorders, and infectious diseases.

Claim 11; Page 177-178; 243pp; English.

XX The invention describes an isolated human secreted HODAZ50 polypeptide
 CC (I) comprising a sequence at least 95% identical to a sequence selected
 CC from polypeptide fragment of any one of the 123 polypeptide sequences
 CC (PS) fully defined in the specification and having biological activity,
 CC polypeptide domain or epitope of PS, secreted form of PS, full-length
 CC protein of PS, or variant, allelic variant or species homologue of PS.
 CC (I) or a polynucleotide (II) encoding (I) is useful for preventing,
 CC treating, or ameliorating a medical condition in a mammalian subject. (I)
 CC or (II) is also useful for diagnosing a pathological condition or a
 CC susceptibility to a pathological condition in a subject. (I) is useful
 CC for identifying a binding partner which involves contacting the
 CC polypeptide with the binding partner and determining whether the binding
 CC partner affects the activity of the polypeptide. (I) or (II) is useful
 CC for diagnosing or treating deficiencies or disorders of the immune
 CC system, deficiencies or disorders of haematopoietic cells, to treat
 CC Wiskott-Aldrich disorders, ataxia telangiectasia, HIV infection,
 CC coagulation disorders, thrombocytopenia or haemoglobinuria, blood
 CC (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis, blood
 CC dermatitis, glomerulonephritis, Grave's disease), allergic reactions,
 CC graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms
 CC located in the abdomen, bone, breast, digestive system, liver, pancreas,
 CC peritoneum, endocrine glands), infectious diseases (e.g., viral,
 CC bacterial, fungal or parasitic infection), central and peripheral nervous
 CC system diseases (e.g., spinal cord disorders, head trauma or stroke), to
 CC differentiate, proliferate and attract cells leading to the regeneration
 CC of tissues to repair, replace or protect tissue damaged by congenital
 CC defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g.,
 CC osteoporosis, periodontal disease, liver failure) or surgery. (I) or (II)
 CC is useful to modulate mammalian characteristics, to modulate mammalian
 CC metabolism affecting catabolism, anabolism, processing, utilisation, and
 CC storage of energy, to change a mammal's mental state or physical state,
 CC or as a food additive or preservative, such as to increase or decrease
 CC storage capabilities, fat content, lipid, protein, carbohydrate,
 CC vitamins, minerals, cofactors or other nutritional components. This is
 CC the amino acid sequence of a novel human secreted protein
 XX Sequence 483 AA;
 SQ

Query Match 77.6%; Score 2509.5; DB 6; Length 483;
 Best Local Similarity 96.9%; Pred. No. 1.3e-224;
 Matches 467; Conservative 2; Mismatches 2; Indels 11; Gaps 1;

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Db	121	SDQREALSHGQNPLPIYCALNTKGQSLITTFEGCEWCEFSPEYVGPYKGFIFSELP	180
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QY	375	LKIEPPPTAGRIAEFFDTLITWRPLAQATNIFLGLHFHKDYFOHPHFSTWATLDG	434
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QY	435	LPNQLTPSPHPLCLLDVGYLINTSCPLLPQTRDVLILSLDYNLHGAFQQLGRFCQ	494
Db	301	LPNQLTPSPHPLCLLDVGYLINTSCPLLPQTRDVLILSLDYNLHGAFQQLGRFCQ	360
QY	495	EGGIFPPPTSPBEOQLQPRECHTSDPTCPGAPAVLHF-----SSGVRRTPEE	543
Db	361	EGGIFPPPTSPBEOQLQPRECHTSDPTCPGAPAVLHFPLVSDSPRESYAGVRRTPEE	420
QY	544	AAAGEVNLSSDSPHYTKVTSQSDVDKLLHLTHYNNVCNQEQLEALRQAVRRQR	603

Fri Oct 8 10:22:32 2004

us-09-830-321a-2.rag

421 AAAGENVLSSDSPHYTKVTYSQEDVDKLLHLYHNCNQLLEALRQVRRQR 480

DB 604 PH 605
QY 481 PH 482
DB

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ID ABO02008 standard; protein; 483 AA.
XX ABO02008;
XX
DT 12-AUG-2003 (first entry)
XX
DE Novel human secreted protein #76.
XX

KW Human; immunoglobulin G; IgG; fragment of crystallisation; FC;
KW immune system disorder; haematopoietic cell disorder;
KW immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
KW Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
KW blood coagulation disorder; blood platelet disorder; autoimmune disorder;
KW Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW Glomerulonephritis; Grave's disease; allergic reaction;
KW graft-versus-host disease; hyperproliferative disorder; neoplasm;
KW infectious disease; nervous system disease; spinal cord disorder;
KW head trauma; stroke; tissue regeneration; congenital defect; trauma;
KW wound; burn; incision; ulcer; age disease; osteoporosis;
KW periodontal disease; liver failure; catabolism; anabolism; metabolism;
KW food additive; preservative; secreted protein.

XX Homo sapiens.
XX
XX US2003027132-A1.
XX
XX 06-FEB-2003.
XX

XX 04-SEP-1998; 98US-00148545.

XX 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
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PR 22-AUG-1997; 97US-0056630P.
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PR 22-AUG-1997; 97US-0056903P.
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PR 22-AUG-1997; 97US-0056910P.
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PR 05-SEP-1997; 97US-0057761P.
PR 06-MAR-1998; 98WO-US004482.
XX
XX (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (FISC/) FISCHER C L.
PA (SOPE/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D R.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
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PA (DUAN/) DUAN R.
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PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DR, Endress GA, Yu G, Ni J, Peng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Shi Y;
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DR WPI; 2003-466138/44.
DR N-PSDB; ACD08100.
XX
PT Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing
PT or treating deficiencies or disorders of the immune system, autoimmune
PT disorders, hyperproliferative disorders, and infectious diseases.
XX
PS Claim 11; Page 210; 243pp; English.

XX The invention describes an isolated human secreted HODAZ50 polypeptide
CC (I) comprising a sequence at least 95% identical to a sequence selected
CC from polypeptide fragment of any one of the 123 polypeptide sequences
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CC polypeptide domain or epitope of PS, secreted form of PS, full-length
CC protein of PS, or variant, allelic variant or species homologue of PS.
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CC polypeptide with the binding partner and determining whether the binding
CC partner affects the activity of the polypeptide. (I) or (II) is useful
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CC system, deficiencies or disorders of haematopoietic cells, to treat
CC immunologic deficiency disorders, ataxia telangiectasia, HIV infection,
CC Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood
CC coagulation disorders, blood platelet disorders, autoimmune disorders
CC (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis,
CC dermatitis, glomerulonephritis, Grave's disease), allergic reactions,
CC graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms
CC located in the abdomen, bone, breast, digestive system, liver, pancreas,
CC peritoneum, endocrine glands), infectious diseases (e.g., viral,
CC bacterial, fungal or parasitic infection), central and peripheral nervous
CC system diseases (e.g., spinal cord disorders, head trauma or stroke), to
CC differentiate, proliferate and attract cells leading to the regeneration
CC of tissues to repair, replace or protect tissue damaged by congenital
CC defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g.,
CC osteoporosis, periodontal disease, liver failure) or surgery. (I) or (II)
CC is useful to modulate mammalian characteristics, to modulate mammalian
CC metabolism affecting catabolism, anabolism, processing, utilisation, and
CC storage of energy, to change a mammal's mental state or physical state,
CC or as a food additive or preservative, such as to increase or decrease
CC storage capabilities, fat content, lipid, protein, carbohydrate,
CC vitamins, minerals, cofactors or other nutritional components. This is
CC the amino acid sequence of a novel human secreted protein

XX Sequence 483 AA;

Query Match 77.6%; Score 2509.5; DB 6; Length 483;
Best Local Similarity 96.9%; Pred. No. 1.3e-224;
Matches 467; Conservative 2; Mismatches 2; Indels 11; Gaps 1;
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Db 121 SDQREALSHGQNPPIYCALNTKGQSLTTFEFGWCEFFSYEVGPKYGFIPSELFGE 180
QY 315 FFMGQLMKRLPESRICFLEGIWSNLVAANLQDSLYWASEPSQFWDWRVNRQANLDEQVP 374
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Db 361 EOGIEPPPTISPSPEQLOPRECHTSDPTCPGAPAVLHP-----SSGVRTPEE 420
QY 544 AAAGEVNLSSDSPHYTKVTYSQEDVDKLLHLTHYVNCNNOELLEALRQAVRRQR 603
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QY 604 PH 605
Db 481 PH 482

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-09-830-321A-2

Perfect score: 3235

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2767.5	85.5	797	US-09-460-145-4	Sequence 4, Appli
4	2767.5	85.5	797	US-09-895-547-4	Sequence 4, Appli
5	2767.5	85.5	913	US-08-827-208-3	Sequence 3, Appli
6	2767.5	85.5	913	US-09-500-358-3	Sequence 3, Appli
7	2767.5	85.5	913	US-09-498-809-3	Sequence 3, Appli
8	2509.5	77.6	483	US-09-148-545-144	Sequence 144, App
9	2509.5	77.6	483	US-09-148-545-209	Sequence 209, App
10	619	19.1	749	US-08-046-508-2	Sequence 2, Appli
11	498.5	15.4	541	US-09-045-185-2	Sequence 2, Appli
12	490.5	15.2	541	US-08-890-615-2	Sequence 2, Appli
13	490.5	15.2	541	US-09-246-290A-2	Sequence 2, Appli
14	208	6.4	638	US-09-687-538B-4	Sequence 2, Appli
15	208	6.4	654	US-09-437-687A-2	Sequence 2, Appli
16	208	6.4	654	US-10-263-250-2	Sequence 2, Appli
17	203.5	6.3	90	US-09-621-976-4397	Sequence 4397, Ap
18	200.5	6.2	640	US-09-687-538B-2	Sequence 2, Appli
19	200	6.2	87	US-09-205-258-342	Sequence 342, App
20	198.5	6.1	66	US-09-621-976-5606	Sequence 5606, App
21	195.5	6.0	552	US-09-295-186-10	Sequence 10, Appl
22	195.5	6.0	573	US-09-295-186-11	Sequence 11, Appl
23	193	6.0	397	PCT-US95-17111A-121	Sequence 121, App
24	189	5.8	117	US-09-621-976-4623	Sequence 4623, Ap
25	188	5.8	627	US-09-687-538B-6	Sequence 6, Appli
26	186.5	5.8	648	US-09-437-687A-16	Sequence 16, Appl
27	186.5	5.8	648	US-10-263-250-16	Sequence 16, Appl

28	185	5.7	375	2	US-08-454-557C-121	Sequence 121, App
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33	177	5.5	612	3	US-09-295-186-16	Sequence 16, Appl
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35	176	5.4	789	4	US-10-020-079-22	Sequence 22, Appl
36	176	5.4	863	4	US-10-020-079-32	Sequence 32, Appl
37	176	5.4	876	4	US-10-020-079-30	Sequence 30, Appl
38	176	5.4	889	4	US-10-020-079-20	Sequence 20, Appl
39	176	5.4	895	4	US-10-020-079-18	Sequence 18, Appl
40	176	5.4	976	4	US-10-020-079-28	Sequence 28, Appl
41	176	5.4	982	4	US-10-020-079-26	Sequence 26, Appl
42	171	5.3	120	4	US-09-621-976-5592	Sequence 5592, App
43	171	5.3	132	4	US-09-636-215-573	Sequence 573, App
44	171	5.3	132	4	US-09-685-166A-573	Sequence 573, App
45	171	5.3	135	4	US-09-685-166A-884	Sequence 884, App

ALIGNMENTS

RESULT 1
US-09-460-145-2
; Sequence 2, Application US/09460145
; Patent No. 6287838
; GENERAL INFORMATION:
; APPLICANT: Kriz, Ron
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,145
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/788,975
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 778 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-460-145-2

Query Match 85.5%; Score 2767.5; DB 3; Length 778;
Best Local Similarity 87.6%; Pred. No. 2.le-268;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

OY 24 TGLIVLFCPCAPCPFFFFFEFMEFSLVAGVQWRDLGSLQPPPLGFKFSCLSLPSWDYR 83

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Db 226 LVFPTSQEPMLRVKKEAGLRLAVLGLGPGCAEQAFLSRRKQVVAALRQALQDGD 285
QY 124 LQDEIPVVAIMATGGGIRAMTSYLGQAGLKEGLDCCVSYITGASGTSWALANLYEDP 183
Db 286 LQDEIPVVAIMATGGGIRAMTSYLGQAGLKEGLDCCVSYITGASGTSWALANLYEDP 345
QY 184 EWSQKDLAGTELLKTQVTKNKLGVLPASQIQRYRQELAEARLGYPSCTFNLWALINEA 243
Db 346 EWSQKDLAGTELLKTQVTKNKLGVLPASQIQRYRQELAEARLGYPSCTFNLWALINEA 405
QY 244 LLHDEPHDKLSQREALSHGQNLPIYCALNTKGQSLTTFEGGECFSEYEVGFPGYK 303
Db 406 LLHDEPHDKLSQREALSHGQNLPIYCALNTKGQSLTTFEGGECFSEYEVGFPGYK 465
QY 304 AFIPSELFGEFFFMGQMLKRLPESRICFLEGIWNSLYAANLQDSLYWASEPSQFWDWRVR 363
Db 466 AFIPSELFGEFFFMGQMLKRLPESRICFLEGIWNSLYAANLQDSLYWASEPSQFWDWRVR 525
QY 364 NQANLDKEQVPLLKIEEPPSTAGIAEFTDILLTWPLAQATHNPLRGLHFKDYFOHPH 423
Db 526 NQANLDKEQVPLLKIEEPPSTAGIAEFTDILLTWPLAQATHNPLRGLHFKDYFOHPH 585
QY 424 FSTWKATTLGIPNQLTSEPHCLLDVGYLINTSCLPLLOTPRDVDLILSLDYNLHGAF 483
Db 586 FSTWKATTLGIPNQLTSEPHCLLDVGYLINTSCLPLLOTPRDVDLILSLDYNLHGAF 645
QY 484 QQLQLLGRFCOEQIGIPFPPIPSPEEQLOPRECHTFSPTCPGAPAVLHF----- 533
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QY 534 -SSGVRRTPEAAAGEVNLSSSDSPYHTKVITYSDVDKLLHLTHYVNCNQEQLLEAL 592
Db 706 SAPGVRRTPEAAAGEVNLSSSDSPYHTKVITYSDVDKLLHLTHYVNCNQEQLLEAL 765
QY 593 RQAVORRRQRPH 605
Db 766 RQAVORRRQRPH 778

RESULT 2

US-09-895-547-2
; Sequence 2, Application US/09895547
; Patent No. 6482625
; GENERAL INFORMATION:
; APPLICANT: Kriz, Ron
; Song, Chuangzheng
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,547
; FILING DATE: 29-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/460,145
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 778 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-895-547-2

Query Match 85.5%; Score 2767.5; DB 4; Length 778;
Best Local Similarity 87.6%; Pred. No. 2.1e-268;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;
QY 24 TGLLVLECPAPCPFFFFEFMESLSVAQAGVQWMDLGSLOPPPLGFKRFSCLSSSSWDYR 83
Db 184 TGTFRHCPA-C-----WEQE-LSI-----RLQDAPBEQLKAPLSALPSGQVVR 225
QY 84 -----LRLAVLGLGPGCAEQAFLSRRKQVVAALRQALQDGD 123
Db 226 LVFPTSQEPMLRVKKEAGLRLAVLGLGPGCAEQAFLSRRKQVVAALRQALQDGD 285
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Db 286 LQDEIPVVAIMATGGGIRAMTSYLGQAGLKEGLDCCVSYITGASGTSWALANLYEDP 345
QY 184 EWSQKDLAGTELLKTQVTKNKLGVLPASQIQRYRQELAEARLGYPSCTFNLWALINEA 243
Db 346 EWSQKDLAGTELLKTQVTKNKLGVLPASQIQRYRQELAEARLGYPSCTFNLWALINEA 405
QY 244 LLHDEPHDKLSQREALSHGQNLPIYCALNTKGQSLTTFEGGECFSEYEVGFPGYK 303
Db 406 LLHDEPHDKLSQREALSHGQNLPIYCALNTKGQSLTTFEGGECFSEYEVGFPGYK 465
QY 304 AFIPSELFGEFFFMGQMLKRLPESRICFLEGIWNSLYAANLQDSLYWASEPSQFWDWRVR 363
Db 466 AFIPSELFGEFFFMGQMLKRLPESRICFLEGIWNSLYAANLQDSLYWASEPSQFWDWRVR 525
QY 364 NQANLDKEQVPLLKIEEPPSTAGIAEFTDILLTWPLAQATHNPLRGLHFKDYFOHPH 423
Db 526 NQANLDKEQVPLLKIEEPPSTAGIAEFTDILLTWPLAQATHNPLRGLHFKDYFOHPH 585
QY 424 FSTWKATTLGIPNQLTSEPHCLLDVGYLINTSCLPLLOTPRDVDLILSLDYNLHGAF 483
Db 586 FSTWKATTLGIPNQLTSEPHCLLDVGYLINTSCLPLLOTPRDVDLILSLDYNLHGAF 645
QY 484 QQLQLLGRFCOEQIGIPFPPIPSPEEQLOPRECHTFSPTCPGAPAVLHF----- 533
Db 646 QQLQLLGRFCOEQIGIPFPPIPSPEEQLOPRECHTFSPTCPGAPAVLHFPLVSDSFREY 705
QY 534 -SSGVRRTPEAAAGEVNLSSSDSPYHTKVITYSDVDKLLHLTHYVNCNQEQLLEAL 592
Db 706 SAPGVRRTPEAAAGEVNLSSSDSPYHTKVITYSDVDKLLHLTHYVNCNQEQLLEAL 765
QY 593 RQAVORRRQRPH 605
Db 766 RQAVORRRQRPH 778

RESULT 3

US-09-460-145-4
; Sequence 4, Application US/09460145
; Patent No. 6287838
; GENERAL INFORMATION:
; APPLICANT: Kriz, Ron
; APPLICANT: Song, Chuangzheng
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9

Db 365 EWSQKLAGTELLKTQVTKNKLGLVLAAPSOLQRYRQELAEARLGYPSCTNLMALINEA 424
QY 244 LLHDEPHDKLSQREALSHGQNPPLIYCALNTKGOSLTTFEGEWCESFYEGFPKYG 303
Db 425 LLHDEPHDKLSQREALSHGQNPPLIYCALNTKGOSLTTFEGEWCESFYEGFPKYG 484
QY 304 AFIPSELFGEFFMGQMLKRLPESRICFLEGIWNLVAANLQDSLYWASESPQWDRWVR 363
Db 485 AFIPSELFGEFFMGQMLKRLPESRICFLEGIWNLVAANLQDSLYWASESPQWDRWVR 544
QY 364 NOANLDEQVPELLKIEPPPPSTAGRIAEFFDTLLTWRLPAQATHNPLRGLHFKHDKYFQHPH 423
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QY 424 FSTWKATTLGDLNQLTPSEPHCLLDVGYLINTSCPLPQTPTRDVLILSLDYNLHGAF 483
Db 605 FSTWKATTLGDLNQLTPSEPHCLLDVGYLINTSCPLPQTPTRDVLILSLDYNLHGAF 664
QY 484 QOLQLGRFCOEQIGIPPPISPSPPEEQLOPRECHTFSDPTCPGAPAVLHF----- 533
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QY 534 -SSGVRRTPEEAAAGEVNLSSDSPYHYTKVYTSQEDVDKLLHLTHYVNCNNQEQLEAL 592
Db 725 SAPGVRRTPEEAAAGEVNLSSDSPYHYTKVYTSQEDVDKLLHLTHYVNCNNQEQLEAL 784
QY 593 RQAVRRRRRRPH 605
Db 785 RQAVRRRRRRPH 797

RESULT 5

US-08-827-208-3
; Sequence 3, Application US/08827208
; Patent No. 6025178
; GENERAL INFORMATION:
; APPLICANT: Chiou, Xue-Chiou C.
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Striffler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,208
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/014,608
; FILING DATE: 29-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,264
; FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756

; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-827-208-3

Query Match 85.5%; Score 2767.5; DB 3; Length 913;
Best Local Similarity 87.6%; Pred. No. 2.7e-268;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;
QY 24 TGLIVLFCPCAPCPFFFEFEMESLSVAQAGVQWRDLGSLQPPPLGFKFSCLSFSSMDYR 83
Db 319 TGTFRFHPA-C-----WEQE-LSI-----RLQDAPEQLKAPLSALFSGQVVR 360
QY 84 -----LRLAVLRLGFGPCABEQAFLSRRKQVVAAALRQALQDGD 123
Db 361 LVFPTSQEPMLMRVELKEAGLRLAVLRLGFGPCABEQAFLSRRKQVVAAALRQALQDGD 420
QY 124 LOEDEIPVVAIMATGGGIRAMTSYLGQLAGLKEGLLDVSYITGASGTWALANLYEDP 183
Db 421 LOEDEIPVVAIMATGGGIRAMTSYLGQLAGLKEGLLDVSYITGASGTWALANLYEDP 480
QY 184 EWSQKLAGTELLKTQVTKNKLGLVLAAPSOLQRYRQELAEARLGYPSCTNLMALINEA 243
Db 481 EWSQKLAGTELLKTQVTKNKLGLVLAAPSOLQRYRQELAEARLGYPSCTNLMALINEA 540
QY 244 LLHDEPHDKLSQREALSHGQNPPLIYCALNTKGOSLTTFEGEWCESFYEGFPKYG 303
Db 541 LLHDEPHDKLSQREALSHGQNPPLIYCALNTKGOSLTTFEGEWCESFYEGFPKYG 600
QY 304 AFIPSELFGEFFMGQMLKRLPESRICFLEGIWNLVAANLQDSLYWASESPQWDRWVR 363
Db 601 AFIPSELFGEFFMGQMLKRLPESRICFLEGIWNLVAANLQDSLYWASESPQWDRWVR 660
QY 364 NOANLDEQVPELLKIEPPPPSTAGRIAEFFDTLLTWRLPAQATHNPLRGLHFKHDKYFQHPH 423
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QY 424 FSTWKATTLGDLNQLTPSEPHCLLDVGYLINTSCPLPQTPTRDVLILSLDYNLHGAF 483
Db 721 FSTWKATTLGDLNQLTPSEPHCLLDVGYLINTSCPLPQTPTRDVLILSLDYNLHGAF 780
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QY 534 -SSGVRRTPEEAAAGEVNLSSDSPYHYTKVYTSQEDVDKLLHLTHYVNCNNQEQLEAL 592
Db 841 SAPGVRRTPEEAAAGEVNLSSDSPYHYTKVYTSQEDVDKLLHLTHYVNCNNQEQLEAL 900
QY 593 RQAVRRRRRRPH 605
Db 901 RQAVRRRRRRPH 913

RESULT 6

US-09-500-358-3
; Sequence 3, Application US/09500358
; Patent No. 6197569
; GENERAL INFORMATION:
; APPLICANT: Chiou, Xue-Chiou C.
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Striffler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company

```

; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,358
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,208
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: US 60/014,608
; FILING DATE: 29-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,264
; FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REFERENCE/DOCKET NUMBER: X-10610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-500-358-3

Query Match 85.5%; Score 2767.5; DB 3; Length 913;
Best Local Similarity 87.6%; Pred. No. 2.7e-268;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

Qy 24 TGLLVLCFPCPFFPFEMESLSVAQAGVQWRDLSLQPPPLGFKRFSCLSLPSSWDYR 83
Db 319 TGTFRFHCPA-C-----WEQE-LSI-----RLQDAPEEQKXAPLSALSGQVVR 360
Qy 84 -----LRELAVRLGFGPCAEQAFLSRRKQVVAALRQALQLDGD 420
Db 361 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEQAFLSRRKQVVAALRQALQLDGD 420
Qy 124 LOEDEIPVATMATGGGIRAMTSYLGQLAGLKGELLDVCVYITGASGSTWALANLYEDP 183
Db 421 LOEDEIPVATMATGGGIRAMTSYLGQLAGLKGELLDVCVYITGASGSTWALANLYEDP 480
Qy 184 EWSQKDLAGTELLKTVTKNKGVLAPSQLRQYQELAEARLGYPCFTNLWALINEA 243
Db 481 EWSQKDLAGTELLKTVTKNKGVLAPSQLRQYQELAEARLGYPCFTNLWALINEA 540
Qy 244 LLHDEPHDKLSQREALSHGONPLIYCALNTKQSLTTFEFGWCWCFSPYEVGFPPKYG 303
Db 541 LLHDEPHDKLSQREALSHGONPLIYCALNTKQSLTTFEFGWCWCFSPYEVGFPPKYG 600
Qy 304 APIPELFGSEFFFMQMKRLPESRICTELEGLWSNLYAANLODSLYWASEPQFWDWVR 363
Db 601 APIPELFGSEFFFMQMKRLPESRICTELEGLWSNLYAANLODSLYWASEPQFWDWVR 660
Qy 364 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRLPQAQTHNPLRGLHFHKDYFOHPH 423
Db 661 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRLPQAQTHNPLRGLHFHKDYFOHPH 720
Qy 424 FSTWKATTDGLPNQLTSPSEPHCLLDVGYLINTSCLPLQPTRDVDVLIISLDYNLHGAF 483
Db 721 FSTWKATTDGLPNQLTSPSEPHCLLDVGYLINTSCLPLQPTRDVDVLIISLDYNLHGAF 780

; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,809
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,809
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,264
; FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REFERENCE/DOCKET NUMBER: X-10610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-498-809-3

Query Match 85.5%; Score 2767.5; DB 3; Length 913;
Best Local Similarity 87.6%; Pred. No. 2.7e-268;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

Qy 24 TGLLVLCFPCPFFPFEMESLSVAQAGVQWRDLSLQPPPLGFKRFSCLSLPSSWDYR 83
Db 319 TGTFRFHCPA-C-----WEQE-LSI-----RLQDAPEEQKXAPLSALSGQVVR 360
Qy 84 -----LRELAVRLGFGPCAEQAFLSRRKQVVAALRQALQLDGD 123

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Db 361 LVFTSDEPLMRVELKKEAGIRELAVRLGRGPCBCEQAFTSRRKQVVAALRQALQDGD 420
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Db 421 LQDEIPVVAIMATGGIRAMTSYLGQAGLKGELGLLDCVSYITGASGSTWALANLYEDP 480
QY 184 EWSQKDLAGTTELLKTQVTKNKLGVLPASQIQRYRQELARARLGYPSCTFNWALINEA 243
Db 481 EWSQKDLAGTTELLKTQVTKNKLGVLPASQIQRYRQELARARLGYPSCTFNWALINEA 540
QY 244 LLHDEPHDKLSDOREALSHGONPLPYCALNTKGOSITTFEGEMWCEFSYEVGPKYG 303
Db 541 LLHDEPHDKLSDOREALSHGONPLPYCALNTKGOSITTFEGEMWCEFSYEVGPKYG 600
QY 304 AFIPSEFGSEFFMGQMLKRLPESRICFLEGIWNLNLYAANLQDSLYWASEPSQFWDWRVR 363
Db 601 AFIPSEFGSEFFMGQMLKRLPESRICFLEGIWNLNLYAANLQDSLYWASEPSQFWDWRVR 660
QY 364 NOANLDEQVPLKIEBPPSTAGRIABFFDTLLTWRLPQAQTHNPLRGLHFKDYFOHPH 423
Db 661 NOANLDEQVPLKIEBPPSTAGRIABFFDTLLTWRLPQAQTHNPLRGLHFKDYFOHPH 720
QY 424 FSTWKATTLGLNPLNPSPHLCCLLDVGYLINTSCLPLLOPTROVDLILSLDYNLHGAF 483
Db 721 FSTWKATTLGLNPLNPSPHLCCLLDVGYLINTSCLPLLOPTROVDLILSLDYNLHGAF 780
QY 484 QQLQLGRFCQEQIPEPPSPSPPEEQIQPRECHTFSDPTCPGAPAVLHF----- 533
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QY 534 -SSQVRTPTEAAAGEVNLSSSDSPHYHTKVTYQSDVDKLLHLTHNVNVCNNQQLLEAL 592
Db 841 SAPGVRRTPTEAAAGEVNLSSSDSPHYHTKVTYQSDVDKLLHLTHNVNVCNNQQLLEAL 900
QY 593 ROAVORRRORRPH 605
Db 901 ROAVORRRORRPH 913

RESULT 8
US-09-148-545-144
; Sequence 144, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 144
; LENGTH: 483

Query Match      77.6%; Score 2509.5; DB 4; Length 483;
Best Local Similarity 96.9%; Pred. No. 7.3e-243;
Matches 467; Conservative 2; Mismatches 2; Indels 11; Gaps 1;

QY 135 MATGGIRAMTSLYGQAGLKEGLDLCVSYITGASGWTWALANLYEDPWSQKDLAAPT 194
DB 1 MATGGIRAMTSLYGQAGLKEGLDLCVSYITGASGWTWALANLYEDPWSQKDLAAPT 60
QY 195 ELLKTQVTKNKLGVLAAPSQIQRYRQELABRARGLPSCFTNLWALINEALLHDEPHDKL 254
DB 61 ELLKTQVTKNKLGVLAAPSQIQRYRQELABRARGLPSCFTNLWALINEALLHDEPHDKL 120
QY 255 SDQREALSHGQNPPIYCALNTKGSLTTFEGWCEWCFSEYEVGPKYGAFFISELFGSE 314
DB 121 SDQREALSHGQNPPIYCALNTKGSLTTFEGWCEWCFSEYEVGPKYGAFFISELFGSE 180
QY 315 FFMGQMLKRLPESRICFLEGIWNSLYAANLQDSLYWASEPSQFWDWRVNRQANLDKEQVP 374
DB 181 FFMGQMLKRLPESRICFLEGIWNSLYAANLQDSLYWASEPSQFWDWRVNRQANLDKEQVP 240
QY 375 LLKIEEPPSTAGRIAEFFTDLLTWRLAQATHNPLRGLHFKDYFOHPHSTWKATTLDG 434
DB 241 LLKIEEPPSTAGRIAEFFTDLLTWRLAQATHNPLRGLHFKDYFOHPHSTWKATTLDG 300
QY 435 LPNLTSEPHLCLLDVGYLINTSCLPLLOPTRDVLILSLDYNLHGAFQQLLGRFCQ 494
DB 301 LPNLTSEPHLCLLDVGYLINTSCLPLLOPTRDVLILSLDYNLHGAFQQLLGRFCQ 360
QY 495 EQGIPFPPIGPSPEEQLPRECHTFSDPTCPGAPAVLHF-----SSGVRRTPEE 543
DB 361 EQGIPFPPIGPSPEEQLPRECHTFSDPTCPGAPAVLHFPLVSDSFREYSAPGVRRTPEE 420
QY 544 AAAGEVNLSSSDSPHYTKVTSQEDVDKLLHLTHYNNCNOEQQLLEALRAQVQRORR 603
DB 421 AAAGEVNLSSSDSPHYTKVTSQEDVDKLLHLTHYNNCNOEQQLLEALRAQVQRORR 480
QY 604 PH 605
DB 481 PH 482

RESULT 9
US-09-148-545-209
; Sequence 209, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001PI
; CURRENT APPLICATION NUMBER: US/09/148,545
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;	EARLIER APPLICATION NUMBER: 60/043,671
;	EARLIER FILING DATE: 1997-04-11
;	EARLIER APPLICATION NUMBER: 60/043,674
;	EARLIER FILING DATE: 1997-04-11
;	EARLIER APPLICATION NUMBER: 60/043,669
;	EARLIER FILING DATE: 1997-04-11
;	EARLIER APPLICATION NUMBER: 60/043,312
;	EARLIER FILING DATE: 1997-04-11
;	EARLIER APPLICATION NUMBER: 60/043,313
;	EARLIER FILING DATE: 1997-04-11
;	EARLIER APPLICATION NUMBER: 60/043,672
;	EARLIER FILING DATE: 1997-04-11
;	EARLIER APPLICATION NUMBER: 60/043,315
;	EARLIER FILING DATE: 1997-04-11
;	EARLIER APPLICATION NUMBER: 60/048,974
;	EARLIER FILING DATE: 1997-06-06
;	EARLIER APPLICATION NUMBER: 60/056,886
;	EARLIER FILING DATE: 1997-08-22
;	EARLIER APPLICATION NUMBER: 60/056,877
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;	EARLIER APPLICATION NUMBER: 60/056,889
;	EARLIER FILING DATE: 1997-08-22
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;	EARLIER FILING DATE: 1997-08-22
;	EARLIER APPLICATION NUMBER: 60/056,845
;	EARLIER FILING DATE: 1997-08-22
;	EARLIER APPLICATION NUMBER: 60/056,892
;	EARLIER FILING DATE: 1997-08-22
;	EARLIER APPLICATION NUMBER: 60/047,595
;	EARLIER FILING DATE: 1997-05-23
;	EARLIER APPLICATION NUMBER: 60/057,761
;	EARLIER FILING DATE: 05-Sep-1997
;	EARLIER APPLICATION NUMBER: 60/047,599
;	EARLIER FILING DATE: 1997-05-23
;	EARLIER APPLICATION NUMBER: 60/047,588
;	EARLIER FILING DATE: 1997-05-23
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;	EARLIER APPLICATION NUMBER: 60/047,586

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
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EARLIER APPLICATION NUMBER: 60/056,881
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 209
LENGTH: 483

Query Match 77.6%; Score 2509.5; DB 4; Length 483;
Best Local Similarity 96.9%; Pred. No. 7.3e-243;
Matches 467; Conservative 2; Mismatches 2; Indels 11; Gaps 1;

QY 135 MATGGIRAMTSLYGQAGLKEGLLDCVSYITGASGSTWALANLYDEPWSQKLAGPT 194
DB 1 MATGGIRAMTSLYGQAGLKEGLLDCVSYITGASGSTWALANLYKDPWSQKLAGPT 60

QY 195 ELKTKQVTKNKLGVLAPOLOQRYQRLAERARLYGSCFTNLWALNEALLHDEPHDKL 254
DB 61 ELKTKQVTKNKLGVLAPOLOQRYQRLAERARLYGSCFTNLWALNEALLHDEPHDKL 120

QY 255 SQREALSHGQNPPIYCAINTKGQSLTTFEGEWCFFSPYEFYKYGAFIPSELFQSE 314
DB 121 SQREALSHGQNPPIYCAINTKGQSLTTFEGEWCFFSPYEFYKYGAFIPSELFQSE 180

QY 315 FPMQMLKLPESRICFLGINSWLYAANLQDSLYWASEPQFWRVNRQANLKEQVP 374
DB 181 FPMQMLKLPESRICFLGINSWLYAANLQDSLYWASEPQFWRVNRQANLKEQVP 240

QY 375 LKIEEPPSTAGRIAEFFTDLLTWRLAQTNPLRGLHFKDYFOHPHSTWKATLLDG 434
DB 241 LKIEEPPSTAGRIAEFFTDLLTWRLAQTNPLRGLHFKDYFOHPHSTWKATLLDG 300

QY 435 LPNQITPSEPHCLLDVGYLINTSCLPLLOPTRDVLILSLDYNLHGAQQQLLGRFCQ 494

DB 301 LPNQITPSEPHCLLDVGYLINTSCLPLLOPTRDVLILSLDYNLHGAQQQLLGRFCQ 360
QY 495 EQGIPPPISPSPERQLOPRECHTFSDPTCPGAPAVLHF-----SSGVRRTPEE 543
DB 361 EQGIPPPISPSPERQLOPRECHTFSDPTCPGAPAVLHFPLVSDSPREYSAPGVRRTPEE 420
QY 544 AAAGEVNLSSSDSPHYHTKVYTSQEDVDKLLHLTHYVNCNQEOLLEALRQAVORRQR 603
DB 421 AAAGEVNLSSSDSPHYHTKVYTSQEDVDKLLHLTHYVNCNQEOLLEALRQAVORRQR 480
QY 604 PH 605
DB 481 PH 482

RESULT 10
US-08-046-508-2
; Sequence 2, Application US/08046508
; Patent No. 5328842
; GENERAL INFORMATION:
; APPLICANT: Chlou et al.
; TITLE OF INVENTION: COMPOUNDS, VECTORS AND METHODS FOR
; TITLE OF INVENTION: EXPRESSING HUMAN CYTOSOLIC PHOSPHOLIPASE A2
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Division/RSM
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,508
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph A. Jones
; REGISTRATION NUMBER: 26,472
; REFERENCE/DOCKET NUMBER: X-8477
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-5183
; TELEFAX: 317-276-1294
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-046-508-2

Query Match 19.1%; Score 619; DB 1; Length 749;
Best Local Similarity 27.1%; Pred. No. 6.9e-53;
Matches 174; Conservative 125; Mismatches 238; Indels 106; Gaps 22;

QY 44 ESLSVAQAGVQWRDLGSLQPPPLGPKRFSCLSPSSWDYRLRELA-----VRLGFGPCABE 99
DB 100 EFLGTATFTVSSMKYGEKEVEFFINQVTEWVLEMS-----LEVSCPLDRFSMALCDE 154

QY 100 QAFLSRRKQVAAALRQAL---QLDGDILQEDDEIPVVAIMATGGIRAMTSLYGQAGLKE 156
DB 155 KTFROQRKEHIRESMKLLGPKNSGLHSARDVPVVAILGSGGFRAMVGFSGVMKALYE 214

QY 157 LGLLDCVSYITGASGSTWALANLYDEPWSQKLAGPTL---LKTQVTKNKLGVLAPO 213
DB 215 SGILPCATYVAAGLSGTMTMTSLYGHDPFPEK---GPEINEELMKNVSHNPLLLTPQK 271

QY 214 LQRYQELAERARLYGSCFTNLWA-LINEALLHDEPHDKLSDQREALSHGQNPPIY 272

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Db 272 VKRYVESLWKKSSQPTFTDIFQMLIGETLIHNRMT-TLSSLUKEKVNTAQCPPLPT 330
Qy 273 ALNTKGQSLTTFEGEWCEFSYVGPYKAFISELFGSEFFMGQMLKRLPESRICFL 332
Db 331 CLHVK-PDVSELMAFDWVEFSYEIGMAKYGTMAPDLFGSKFFGTGVVKKYEENPHFL 389
Qy 333 EGIWENLYA-----ANLQDSLYWASEPSQFWDWRVRNQANLDKQVPL 376
Db 330 MGWCSARSILNVLVSGSQSRGSTWEEEL-----ENITTKHIVNSDSDSD 439
Qy 377 KIEEPPSTAGRIA--EFTFD-----LLTWRPLAQATHNFLRGLHPH 415
Db 440 ESHEPKGTENEDAGSDYQSDNQASWHRMIMALVSDSALFNTRGKAGKVNFMGLNLN 499
Qy 416 KDYFOHP--HSTWKAATILDGL-----PNQ-----LTPSEPHCLLDVGYLNTSCL 460
Db 500 TSYPLSPLSDFATQDSFDDDELDAADPDEFERIEPLDVKSXKHVVDSGLTFLNLPY 559
Qy 461 PLLQPTRDVLILSLDYNLHGA-----FQQLQLGRFCQEQIPIPPPIPSPEEQLOPRE 515
Db 560 LILRQGVDLIISDFARSPPSPFKELLALAEKWKAKMNLPPKIDPYVFDREGLKE 619
Qy 516 CHTFSDPTCP-----CAPAVLHF-----SSGV-RTTPEAAAGVNL-SSSDSPY 558
Db 620 CVYFK-PKNPDMKDCPTIHFVLANINPRKYKAPGVPRETEEKEIADFIDDPESPF 678
Qy 559 HYTKVYTSQEDVKLLHLTHYVNCNQEQLLEALQCAVQRREQ 601
Db 679 STNFQYENQAFKRLHLMHFNLTANNIDIVKEAMVESIEYRQ 721

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RESULT 11

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US-09-045-185-2
; Sequence 2, Application US/09045185
; Patent No. 6103510
; GENERAL INFORMATION:
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Strifler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,185
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: P-11369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-09-045-185-2

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Query Match 15.4%; Score 498.5; DB 3; Length 541;
Best Local Similarity 27.8%; Pred. No. 4.9e-41;
Matches 158; Conservative 86; Mismatches 190; Indels 135; Gaps 23;
Qy 98 BEQAFLSRRKQVVAALRQALQDGLQDEIPVVAIMATGGIRAMTSLYQQLAGLKL 157
Db 15 EEKAVERRRHLVLKALKL-----RIEADAFVAVVLGSGGGLRAHIACTGLVSEMKEQ 69
Qy 158 GLLDVCVSIITGASGTWALANIYE---DPEWSQKDLAGTELLKTQVTKNKLGVLAPOSQ 214
Db 70 GLLDVAVTVIAGVSGTWAISLTYTNDGMEALEAD-----LKRFRTRQEW-----DL 116
Qy 215 QRYRQELAEARLGYPSCTNLWA-LINEALLHDSPHDKLSDOREALSHGQNPLPIYCA 273
Db 117 AKSLQKTQAARSENYS-LTDFWAMVVISKQTRULPESH-LSNMKKPVEEGTLPIPIFAA 174
Qy 274 ----INTKGQSLTTFEGEWCEFSYVGPYKAFIPSELPFGSEFFMGQMLKRLPESRI 329
Db 175 IDNDLQPSWQEARAPE--TWFEFTPHAGFPALGAFVSIHFSGFKKGLRVRTHTPERDL 232
Qy 330 CFLEGIWNS-----LYA--ANLQDSLY 349
Db 233 TELRLGWSALGNTVEIREYIFDQURNLTLKGLMRRANAKSIGHLIFARLLRQESQ 292
Qy 350 W-----AGEPSQFW-----DRVRNQANLDKQVPLLKTEEPSTAGRIAEPF---- 392
Db 293 GEHPPEDEGEPEHTWLTLENWTR--TSLEKQEQP-----HEDPERKGSLSNLMDFVK 346
Qy 393 -TDLLTWRPLAQATHNFLRGLHFKDYFOHPHFSTWKATTLDGLPNQLTPSEPHCLLDV 451
Db 347 KTGICASKWEGTTHNFL-----YKH-----GGIRDKIMSSRKKHLHLVDA 386
Qy 452 GYLINTSCLPLQPTDVLILSLDYNLHGAFOQLQLGRFCQEQIPIPPPIPSPEEQLO 511
Db 387 GLAINTFPFLVLPPTREVHLILSDFDSAGDPETIRATTDYCRRHKIPFPQVE--EABL 443
Qy 512 Q-----PRECHTFSDPTCPGAPAVLHFSSGVRRTP---EAAAAGEVNLSSSDSPYHYTKV 563
Db 444 DLMSKAPASCYLKGET---GPVVMHF-----PLENIDAGGDLAEWSDTYDIFKLAD 493
Qy 564 TYSQBEDVKLLHLTHYVNCNQEQLLEAL 592
Db 494 TYTLDVWVLLALAKKNVRENKKILREL 522

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RESULT 12

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US-08-890-615-2
; Sequence 2, Application US/08890615
; Patent No. 6121031
; GENERAL INFORMATION:
; APPLICANT: Song, Chuansheng
; APPLICANT: Kriz, Ron
; APPLICANT: Knopf, John
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-GAMMA ENZYMES
; TITLE OF INVENTION: AND POLYNUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,615
; FILING DATE:

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G1300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8224
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Active-site
LOCATION: 6..242
FEATURE:
NAME/KEY: Active-site
LOCATION: 366..535
US-08-890-615-2

Query Match 15.2%; Score 490.5; DB 3; Length 541;
Best Local Similarity 27.6%; Pred. No. 3.1e-40;
Matches 157; Conservative 86; Mismatches 191; Indels 135; Gaps 23;

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Db 15 EKAVERRRRLHLKALKKL-----RIEADAPVAVVLGGGGLRAHIAICLVLSMKEQ 69

QY 158 GLLDVCYSITGASGTSWALANLYE---DPEWSOKLAGTTELLKTQVTKNKLGVLA 214
Db 70 GLLDVAVTLGAVSGTSWALSSLYTNDGMEALD-----LKHFTQEW-----DL 116

QY 215 QYRQELAEARALGVPSCFTNLWA-LINEALLHDEPHDKLSQREALSHGONPLPIYCA 273
Db 117 AKSLQKTIQAARSENYS-LTDFWAYVVISKQRELPEH-LSNMKKPVVEGTLPIYPIAA 174

QY 274 ----LNTKQSLTTFEGWCSEFSPVEGPKYGFIPSELFGSEFFMGQMKMLPESRI 329
Db 175 INDNLQPSQWEARPE--TWFEFTPHAGFSALGAFVSTHFGSKFKGRLVTRTHPERDL 232

QY 330 CFLEGISWN-----LVA--ANLQDSLY 349
Db 233 TFLRGLWSALGNTEVIREYIFDQLRNLTGLMRRANAKSIGHLIFARLLRLQESSQ 292

QY 350 W-----ASPSQFW-----DRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFF--- 392
Db 293 GEHPPEDEGGPEHTWLTLEMLNTR--TSLEKQEQP---HEDPERKGSLSNLMDFVK 346

QY 393 -TDLLTWRPLAQATHNPLRGLHFHKDYFOHPHFSTWKTATLDGLPNQLTPSEPHCLLDV 451
Db 347 KTGICASKWEGTTHNPL-----YKH-----GGIRDKIMSSRRKHLHVD 386

QY 452 GYLINTSCLPLLOPTRDVLILSDYNLHGAFQQLQLGRFCQEQGIPPPISPSPEOL 511
Db 387 GLAINTPPLVLPPTREVHLLISDFESAGDPETIRATTDYCRHKIPPPQVE---EAL 443

QY 512 Q-----PRECHTFSPTCPGAPAVLHFSFGVRRTP---EAAAGEVNLSSSDSPHYTKV 563
Db 444 DLWSKAPASCYILKGET---GPVVIHF-----PLFNIDACGGDIEAWSDTYDTFKLAD 493

QY 564 TYSQEDVDKLLHLTHYVNCNQEQQLLEAL 592
Db 494 TYTLDDVVVLLALAKKNVRENKKILREL 522
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RESULT 13
US-09-246-290A-2
Sequence 2, Application US/09246290A
Patent No. 6440683
GENERAL INFORMATION:

APPLICANT: Song, Chuanzheng
APPLICANT: Kriz, Ronald
APPLICANT: Knopf, John
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-GAMMA ENZYMES
FILE REFERENCE: AND POLYNUCLEOTIDES ENCODING SAME
CURRENT APPLICATION NUMBER: US/09/246,290A
CURRENT FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: US 08/890,615
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 541
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: ACT_SITE
LOCATION: (6)....(242)
NAME/KEY: ACT_SITE
LOCATION: (366)....(535)
US-09-246-290A-2

Query Match 15.2%; Score 490.5; DB 4; Length 541;
Best Local Similarity 27.6%; Pred. No. 3.1e-40;
Matches 157; Conservative 86; Mismatches 191; Indels 135; Gaps 23;

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QY 98 EQAFLSRRKQVVAALRQALQDGLDQDEIPVVAIMATGGIRAMTSLYQGLAGLKE 157
Db 15 EKAVERRRRLHLKALKKL-----RIEADAPVAVVLGGGGLRAHIAICLVLSMKEQ 69

QY 158 GLLDVCYSITGASGTSWALANLYE---DPEWSOKLAGTTELLKTQVTKNKLGVLA 214
Db 70 GLLDVAVTLGAVSGTSWALSSLYTNDGMEALD-----LKHFTQEW-----DL 116

QY 215 QYRQELAEARALGVPSCFTNLWA-LINEALLHDEPHDKLSQREALSHGONPLPIYCA 273
Db 117 AKSLQKTIQAARSENYS-LTDFWAYVVISKQRELPEH-LSNMKKPVVEGTLPIYPIAA 174

QY 274 ----LNTKQSLTTFEGWCSEFSPVEGPKYGFIPSELFGSEFFMGQMKMLPESRI 329
Db 175 INDNLQPSQWEARPE--TWFEFTPHAGFSALGAFVSTHFGSKFKGRLVTRTHPERDL 232

QY 330 CFLEGISWN-----LVA--ANLQDSLY 349
Db 233 TFLRGLWSALGNTEVIREYIFDQLRNLTGLMRRANAKSIGHLIFARLLRLQESSQ 292

QY 350 W-----ASPSQFW-----DRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFF--- 392
Db 293 GEHPPEDEGGPEHTWLTLEMLNTR--TSLEKQEQP---HEDPERKGSLSNLMDFVK 346

QY 393 -TDLLTWRPLAQATHNPLRGLHFHKDYFOHPHFSTWKTATLDGLPNQLTPSEPHCLLDV 451
Db 347 KTGICASKWEGTTHNPL-----YKH-----GGIRDKIMSSRRKHLHVD 386

QY 452 GYLINTSCLPLLOPTRDVLILSDYNLHGAFQQLQLGRFCQEQGIPPPISPSPEOL 511
Db 387 GLAINTPPLVLPPTREVHLLISDFESAGDPETIRATTDYCRHKIPPPQVE---EAL 443

QY 512 Q-----PRECHTFSPTCPGAPAVLHFSFGVRRTP---EAAAGEVNLSSSDSPHYTKV 563
Db 444 DLWSKAPASCYILKGET---GPVVIHF-----PLFNIDACGGDIEAWSDTYDTFKLAD 493

QY 564 TYSQEDVDKLLHLTHYVNCNQEQQLLEAL 592
Db 494 TYTLDDVVVLLALAKKNVRENKKILREL 522
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RESULT 14
US-09-687-538B-4
Sequence 4, Application US/09687538B
Patent No. 6514739
GENERAL INFORMATION:

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; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Frandsen, Torben
; APPLICANT: Nielsen, Tom
; APPLICANT: Kauppinen, Markus
; APPLICANT: Christensen, Soeren
; TITLE OF INVENTION: Lysophospholipase
; FILE REFERENCE: 5958.210-US
; CURRENT APPLICATION NUMBER: US/09/687,538B
; CURRENT FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-687-538B-4

Query Match      6.4%; Score 208; DB 4; Length 638;
Best Local Similarity 20.1%; Pred. No. 9e-12;
Matches 108; Conservative 74; Mismatches 156; Indels 200; Gaps 26;

QY 129 IPVVAIMATGGIRAMTSLYGQAGLKE-----GLDCVSYITGASGSTMALA 177
Db 114 IPNIAAASGGYRALTGAGALKAFDSRSDNATNSGQGLGQAAATVYSGLSGWSLVG 173
QY 178 NLY-----EDPEWSQKDLAQPTELLKTQVTKNKLGLVLAPSQ 213
Db 174 SMFVNFSIGELQASEKVMRFDKSLLEGPNFDHIQIVSTVEYWK-DIT----- 221
QY 214 LQRYQELAEARLGPSCFTNLWA-----LINE-----ALLHDPHDK 253
Db 222 -----EVDGKANAGFNTSFTDYWGRALSYQLVNASDDKGGPDYTWSSIALMDD----- 270
QY 254 LSDQREALSHGQNPPIYCA-LNTGQ-----SLTTFRGEWCESPYEVGPKYGATP 307
Db 271 -----FKNGYPMPIVVADGRNPGELIIVETNATVIEVNPW-BFGSPD-----PSVAFAP 319
QY 308 SELFGESEFMGLKMLPESRIC-----FLEGIWSNLYAANLQDSLYWASEPSQWD 359
Db 320 LQYLSGRFENG-----IPNGICVSGFDNAGFMGSSSLF-----NQF-- 359
QY 360 RWRNQAANDKQVPLKIEBPSTAGTAEFTDLLTRPLAQATHNLRGLHFHKDYF 419
Db 360 -----LLQINSTSIEPT-----LKDAFTDIL-EDLGERNDIT-----AVYS 394
QY 420 QHPFSTWKATTLDELGNLQPTSEPHLCILDVGYL-----INTSCLPLLOPTRDVLL 473
Db 395 PNP-FSGYADS-----SEDYATAKDLVDVCGEDGENIPLHPLIQPERAVDVIF 442
QY 474 SLDYNLHGAF---QQLGLGRFCQEQGIPPPPIPSPEBQLOPFBRECHTESDPTCPGAPAV 530
Db 443 AIDSSADTDYWPNGTSLVATY-----ERSLEPSIANGTAFPAVPDQNTF 487
QY 531 LHFSSGVRTPTEAAGAVNLSS-----DSPHYT-----KVYSQEDVDKLL 574
Db 488 VNL--GLNSRPTFFGCDPKNISGTAPLVLYLPNSPYTDSNFSFTKLITSDEERDSVI 543
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RESULT 15

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US-09-437-687A-2
; Sequence 2, Application US/09437687A
; Patent No. 6489154
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Tony Byun
; APPLICANT: Ryoko Itami
; APPLICANT: No. 6489154iko Tsutsumi
; TITLE OF INVENTION: Polypeptides Having Lysophospholipase
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5713.200-US
; CURRENT APPLICATION NUMBER: US/09/437,687A
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; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/189,486
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Fusarium venenatum
US-09-437-687A-2
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Query Match      6.4%; Score 208; DB 4; Length 654;
Best Local Similarity 21.7%; Pred. No. 9.4e-12;
Matches 146; Conservative 82; Mismatches 216; Indels 230; Gaps 35;
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QY 36 PFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKFSCLSLPSS-----WDYRLRE 86
Db 4 PLVFTLWITSSAIAAPD-----DAGLVAAPATG-KSLSTRALPDSGGYAPKVVDCPSTR 58
QY 87 LAVRLGFGPCABEQAFLSRRKQVAAALRQALQ-----LDGD--LQDE-----IPVVA 133
Db 59 PKIRLADGLSDQEEAWVRNRNTIDPMKDLLSRVNISGFDKAEKWKNNKNNATALPNA 118
QY 134 IMATGGIRAMTSLYGQAGLKE-----GLDCVSYITGASGSTMALANLVED--- 182
Db 119 IAASGGYRALMNGAGFTISAADSRNNEGPIISGLQSSSTYLQSLGSGGWLVSIFANNPT 178
QY 183 --PEWSQK-----LAGPTELLKTQVTKNKLGLVLAPSOLQRYROELAEARARUG 228
Db 179 TPTDLOKDGSDIWAFRSIFKGP-----EASGLNVLNTAKYWDIDKDTVEKADG 230
QY 229 YPSCFTNLWALINEALLHDEPHDKLSQREA-----LHGQNPLPIYCA- 273
Db 231 WNTTLDWM--GRAL-----SYQLIDASEGGPAYTFSSIADTSNFKDADTPFPLVAD 281
QY 274 -----LNTKQSLTTFEFGWCESPYEVGPKYGATIPSELPSEBFFMGOLMKR 323
Db 282 GRAPQQRIVSLNATVYFNPFEFGTWDPTS-----YG-FAPVEYIGSNFTNGTIEK- 331
QY 324 LPESRIC-----FLEGIWSNLYAANLQDSLYWASEPSQWDRWRNQAANDKEQVPL 375
Db 332 ---GGECVRGFPQFGVMTSSSLFNQFLNNITKIGE-----ENDIES 372
QY 376 LKIEPPPTAGRIAEFTDLLTRPLAQATHNLRGLHFH-----KDYFOHPHFSTWKAT- 430
Db 373 L-----VVKAIQGLFVALDITNDEDIADYSNP-FYQWNVVG 407
QY 431 -TLDGLPNQLTSEPHLCILDVGY-LINTSCLPLLOPTRDVLLILSDYN----- 478
Db 408 KSYNAKDHQLT-----LVQGGEDLQNIPLHPLIQVRGVDIIFAISSADTDNNWPN 460
QY 479 --LHGAFQOL-QLLGRFCQEQGIPPPPIPSPE-----EOLOPR-----ECHTFSDPT 523
Db 461 TALARATYDRVDSLSG-----NGTQFPST-PSAETFINEKLNQRPITLFGCDADNFTLSDCK 514
QY 524 CPGAPAVLHFSSGVRTPTEAAGAVNLSSSDSPHYTKVYSQEDVDKLLHLYNVN 583
Db 515 AP-PPLVFI-----PNAPYTFLSNVSTFD-----LSYSIPERDSI----- 549
QY 584 NOEQLEALLRQAVQ 597
Db 550 ----ILNALNGATQ 559
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Search completed: October 5, 2004, 19:24:58
Job time : 41.9133 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 19:25:05 ; Search time 137.133 Seconds
(without alignments)
1419.702 Million cell updates/sec

Title: US-09-830-321A-2

Perfect score: 3235

Sequence: 1 MIFVELSPITALCLERVASH.....EQLLEALRQAVQRRRRQRP 605

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2767.5	85.5	778	14	US-10-266-388-2
2	2767.5	85.5	797	14	US-10-266-388-4
3	2767.5	85.5	1012	16	US-10-408-765A-638
4	2509.5	77.6	483	9	US-09-981-876-144
5	2509.5	77.6	483	9	US-09-981-876-209
6	2509.5	77.6	483	10	US-09-148-545-144
7	2509.5	77.6	483	10	US-09-148-545-209
8	1492	46.1	1026	12	US-10-332-426-6
9	1243.5	38.4	996	16	US-10-467-248-1
10	1139.5	35.2	849	15	US-10-380-873B-1
11	1138	35.2	853	15	US-10-380-873B-38
12	1127	34.8	854	15	US-10-380-873B-22
13	1112	34.4	848	12	US-10-332-426-3
14	619	19.1	749	12	US-10-211-462-50
15	619	19.1	749	12	US-10-157-898-2

16	619	19.1	749	13	US-10-062-730-2	Sequence 2, Appli
17	619	19.1	749	14	US-10-021-660-118	Sequence 118, App
18	593.5	18.5	748	12	US-10-157-898-4	Sequence 4, Appli
19	490.5	15.2	541	12	US-10-211-462-93	Sequence 93, Appli
20	490.5	15.2	541	14	US-10-021-660-127	Sequence 127, App
21	490.5	15.2	541	16	US-10-741-601-296	Sequence 296, App
22	490.5	15.2	541	16	US-10-741-601-297	Sequence 297, App
23	461	14.3	597	14	US-10-181-612-4	Sequence 4, Appli
24	419	13.0	180	12	US-10-296-115-917	Sequence 917, App
25	368.5	11.4	261	15	US-10-380-873B-26	Sequence 26, Appli
26	361	11.2	454	15	US-10-380-873B-3	Sequence 3, Appli
27	358	11.1	442	16	US-10-468-519-1	Sequence 1, Appli
28	347.5	10.7	441	16	US-10-468-519-8	Sequence 8, Appli
29	344	10.6	445	16	US-10-468-519-5	Sequence 5, Appli
30	339	10.5	384	16	US-10-741-601-295	Sequence 295, App
31	232	7.2	151	14	US-10-017-161-1210	Sequence 1210, Ap
32	232	7.2	151	15	US-10-292-798-1020	Sequence 1020, Ap
33	220	6.8	150	15	US-10-094-749-1682	Sequence 1682, Ap
34	217	6.7	135	12	US-10-424-599-242280	Sequence 242280,
35	216	6.7	101	15	US-10-094-749-2181	Sequence 2181, Ap
36	211	6.5	137	12	US-10-276-774-1959	Sequence 1959, Ap
37	211	6.5	157	15	US-10-108-260A-4272	Sequence 4272, Ap
38	210	6.5	157	12	US-10-276-774-1940	Sequence 1940, Ap
39	208.5	6.4	137	12	US-10-276-774-1949	Sequence 1949, Ap
40	208.5	6.4	183	9	US-09-989-920-245	Sequence 245, App
41	208.5	6.4	361	9	US-09-995-494-107	Sequence 107, App
42	208	6.4	97	12	US-10-276-774-2008	Sequence 2008, Ap
43	208	6.4	638	14	US-10-309-437-4	Sequence 4, Appli
44	208	6.4	654	14	US-10-263-250-2	Sequence 2, Appli
45	206	6.4	213	12	US-10-296-115-911	Sequence 911, App

ALIGNMENTS

RESULT 1
US-10-266-388-2
; Sequence 2, Application US/10266388
; Publication No. US20030124702A1
; GENERAL INFORMATION:
; APPLICANT: Kriz, Ron
; Song, Chuansheng
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/266,388
; FILING DATE: 07-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,547
; FILING DATE: 29-Jun-2001
; APPLICATION NUMBER: 09/460,145
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 778 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-266-388-2

Query Match      85.5%; Score 2767.5; DB 14; Length 778;
Best Local Similarity 87.6%; Pred. No. 1.2e-254;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

QY 24 TGLLVLPFCAPCPFFPFEMESLSVAQAGVQWMDLGSLOPPPLGPKRFSCLSLPSSWDYR 83
DB 184 TGTRFHCFA-C-----WEQE-LST-----RLQDAPEEQKAPLSALPSGVVR 225

QY 84 -----LRELAVRLGFGPCABEQAFLSRRKQVAAALRQALQLDGD 123
DB 226 LVFPTSQELMRVELKKEAGRELAVRLGFGPCABEQAFLSRRKQVAAALRQALQLDGD 285

QY 124 LOEDBIPVVAIMATGGIRAMTSYGLAGLKGELGLDCVSYITGASGSTWALANLYRDP 183
DB 286 LOEDBIPVVAIMATGGIRAMTSYGLAGLKGELGLDCVSYITGASGSTWALANLYRDP 345

QY 184 EWSQKDLAAGPTTELLKTQVTKNKGVLAPSQLQRYQELAEARLGYPCFTNLWALINEA 243
DB 346 EWSQKDLAAGPTTELLKTQVTKNKGVLAPSQLQRYQELAEARLGYPCFTNLWALINEA 405

QY 244 LLHDEPHDKLSQDREALSHGONPLPIYCALNTKGOSLTTFEFGWCFSFVEVGFPKYG 303
DB 406 LLHDEPHDKLSQDREALSHGONPLPIYCALNTKGOSLTTFEFGWCFSFVEVGFPKYG 465

QY 304 AFIPSELFSGSFFFMQMLKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFMDRWR 363
DB 466 AFIPSELFSGSFFFMQMLKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFMDRWR 525

QY 364 NOANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRLAQATHNPLRGLHFKHGYFQHPH 423
DB 526 NOANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRLAQATHNPLRGLHFKHGYFQHPH 585

QY 424 PSTWKATTLTDLGNLTSEPHCLLDVGYLINTSCLPLQPTDRDVLILSLDYNLHGAF 483
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QY 484 QQLQLGRFCOEQGIPIPPPIGSPSEQLQPRECHTFSDPTCPGAPAVLHF----- 533
DB 646 QQLQLGRFCOEQGIPIPPPIGSPSEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 705

QY 534 -SSGVRRTPEAAAGEVNLSSSDSPYHTKVTYSQEDVDKLLHLTHYNVNCNQEQLLEAL 592
DB 706 SAPGVRRTPPEAAAGEVNLSSSDSPYHTKVTYSQEDVDKLLHLTHYNVNCNQEQLLEAL 765

QY 593 QAVQRRRRQRPH 605
DB 766 QAVQRRRRQRPH 778

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RESULT 2

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US-10-266-388-4
; Sequence 4, Application US/10266388
; Publication No. US20030124702A1
; GENERAL INFORMATION:
; APPLICANT: Kriz, Ron
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/266,388
; FILING DATE: 07-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,547
; FILING DATE: 29-Jun-2001
; APPLICATION NUMBER: 09/460,145
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 777 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-266-388-4

Query Match      85.5%; Score 2767.5; DB 14; Length 797;
Best Local Similarity 87.6%; Pred. No. 1.2e-254;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

QY 24 TGLLVLPFCAPCPFFPFEMESLSVAQAGVQWMDLGSLOPPPLGPKRFSCLSLPSSWDYR 83
DB 203 TGTRFHCFA-C-----WEQE-LST-----RLQDAPEEQKAPLSALPSGVVR 244

QY 84 -----LRELAVRLGFGPCABEQAFLSRRKQVAAALRQALQLDGD 123
DB 245 LVFPTSQELMRVELKKEAGRELAVRLGFGPCABEQAFLSRRKQVAAALRQALQLDGD 304

QY 124 LOEDBIPVVAIMATGGIRAMTSYGLAGLKGELGLDCVSYITGASGSTWALANLYRDP 183
DB 305 LOEDBIPVVAIMATGGIRAMTSYGLAGLKGELGLDCVSYITGASGSTWALANLYRDP 364

QY 184 EWSQKDLAAGPTTELLKTQVTKNKGVLAPSQLQRYQELAEARLGYPCFTNLWALINEA 243
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QY 304 AFIPSELFSGSFFFMQMLKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFMDRWR 363
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QY 364 NOANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRLAQATHNPLRGLHFKHGYFQHPH 423
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QY 424 PSTWKATTLTDLGNLTSEPHCLLDVGYLINTSCLPLQPTDRDVLILSLDYNLHGAF 483
DB 605 PSTWKATTLTDLGNLTSEPHCLLDVGYLINTSCLPLQPTDRDVLILSLDYNLHGAF 664

QY 484 QQLQLGRFCOEQGIPIPPPIGSPSEQLQPRECHTFSDPTCPGAPAVLHF----- 533
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 ; NUMBER OF SEQ ID NOS: 280
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 144
 ; LENGTH: 483

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 Best Local Similarity 96.9%; Pred. No. 2.4e-230;
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QY 255 SDOREALSHGQNPPIYCALNTKGQSLTTFEGWCEFSFYEVGPKYGAFIPSELFSGE 314
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Db 121 SDOREALSHGQNPPIYCALNTKGQSLTTFEGWCEFSFYEVGPKYGAFIPSELFSGE 180
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QY 315 FWMQMKELPESRICFLEGIWSNLNLAQSLYASPSQFWDNRVNRQANLDKEQVP 374
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QY 604 PH 605
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Db 481 PH 482

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; Sequence 209, Application US/09981876
; Patent No. US2002016469A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 209
; LENGTH: 483

Query Match      77.6%; Score 2509.5; DB 9; Length 483;
Best Local Similarity 96.9%; Pred. No. 2.4e-230;
Matches 467; Conservative 2; Mismatches 2; Indels 11; Gaps 1;

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001PI
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
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67	EARLIER FILING DATE: 1997-05-23
68	EARLIER APPLICATION NUMBER: 60/047,586
69	EARLIER FILING DATE: 1997-05-23
70	EARLIER APPLICATION NUMBER: 60/047,590
71	EARLIER FILING DATE: 1997-05-23
72	EARLIER APPLICATION NUMBER: 60/047,594
73	EARLIER FILING DATE: 1997-05-23


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; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
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; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
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; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 209
; LENGTH: 483

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Query Match 77.6%; Score 2509.5; DB 10; Length 483;
 Best Local Similarity 96.9%; Pred. No. 2.4e-230;
 Matches 467; Conservative 2; Mismatches 11; Gaps 1;

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Db 1 MATGGIRAMTSLYQGLAGKELGLDCXSYITGASGTSWALANLYKDPWSDKLAGPT 60
Qy 195 ELLKTQVTKNKLGVLPAPSOLORYQELAEARLGYBSCFTNLWALINEALLHDPHDHKL 254
Db 61 ELLKTQVTKNKLGVLPAPSOLORYQELAEARLGYBSCFTNLWALINEALLHDPHDHKL 120
Qy 255 SDQREALSHGQNPPIYCALNTKQSLTTFBFGWCEPSPYEVGPKYGAFTPSLFGSE 314
Db 121 SDQREALSHGQNPPIYCALNTKQSLTTFBFGWCEPSPYEVGPKYGAFTPSLFGSE 180
Qy 315 FFMQMLKRLPESRICFLEGWNSNLYAANLQDSLYWASEPQFMDRWVRNQNALDKQVP 374
Db 181 FFMQMLKRLPESRICFLEGWNSNLYAANLQDSLYWASEPQFMDRWVRNQNALDKQVP 240
Qy 375 LKTEEPSTAGRTAEFTDILLTWPLAQATHNLFRLGHFKHDXFQHPHSTWKAATLDG 434
Db 241 LKTEEPSTAGRTAEFTDILLTWPLAQATHNLFRLGHFKHDXFQHPHSTWKAATLDG 300
Qy 435 LPNOLTPSEPHCLLDVGYLINTSCPLPQLQPTRDVLILSLDYNLHGAFQQLLGRFCQ 494
Db 301 LPNOLTPSEPHCLLDVGYLINTSCPLPQLQPTRDVLILSLDYNLHGAFQQLLGRFCQ 360
Qy 495 EQGIPFPISPSPEQLQPRECHTSDPTCPGAPAVLHP-----SSGVRTPEE 543
Db 361 EQGIPFPISPSPEQLQPRECHTSDPTCPGAPAVLHP-----SSGVRTPEE 420
Qy 544 AAGGVNLSSDSPHYTKVTSQSDVDKLLHLTHYVNCNNOELLEALROAVRRORR 603
Db 421 AAGGVNLSSDSPHYTKVTSQSDVDKLLHLTHYVNCNNOELLEALROAVRRORR 480
Qy 604 PH 605
Db 481 PH 482
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RESULT 8

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US-10-332-426-6
; Sequence 6, Application US/10332426
; Publication No. US20040029136A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; DAS, Debopriya;
; APPLICANT: THORNTON, Michael; LU, Dyung Aina M.;
; APPLICANT: TRIBOULEY, Catherine M.; YUE, Henry;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
; APPLICANT: KHAN, Farrah A.; LU, Yan;
; APPLICANT: YAO, Monique G.; HAFALIA, April J. A.;
; APPLICANT: ELLIOTT, Vicki S.; ARVIZU, Chandra S.;
; APPLICANT: LAL, Preeti; RAMKUMAR, Jayalaxmi;
; APPLICANT: NGUYEN, Daniel B.; BAUGHN, Mariah R.
; TITLE OF INVENTION: LIPID METABOLISM MOLECULES
; FILE REFERENCE: PI-0152 USN
; CURRENT APPLICATION NUMBER: US/10/332,426
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/216,803
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/216,801
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/218,233
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/220,046
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,739
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/222,824
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 1026
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040029136A1 7477093CD1
US-10-332-426-6
Query Match 46.1%; Score 1492; DB 12; Length 1026;
Best Local Similarity 51.6%; Pred. No. 1.3e-13;
Matches 296; Conservative 92; Mismatches 152; Indels 34; Gaps 8;
Qy 61 LOPPLGPKFSCSLSPSSWDYRLR-----ELAVRLGFGPCAEQAFLSRRKQVAA 112
Db 452 LRPLTIGKVTMDYPAFNAQVRLQLKAEQCEELAVHLGFLNCAEQAFLSRRKQVAK 511
Qy 113 ALRQALQDLQDEDEIPVVAIMATGGIRAMTSYQGLAGKELGLDCCVSYITGASG 172
Db 512 ALKQALQDLQDEDEIPVVAIMATGGIRAMTSYQGLAGKELGLDCCVSYITGASG 571
Qy 173 TWALANLYYEDPEWSQDLAGTELLKTQVTKNKLGVLPAPSOLORYQELAEARLGYBSC 232
Db 572 TWTWAHLVGDPEWSQDLAGTELLKTQVTKNKLGVLPAPSOLORYQELAEARLGYBSC 631
Qy 233 FTNLWALINEALLHDPHDHKLSDQREALSHGQNPPIYCALNTKQSLTTFBFGWCEP 292
Db 632 FVDLWALVLESMLHGQVMDQKLSQRAALRGQNPPLVLSLVKNNLETLDFKEMVEF 691
Qy 293 SPYEVGPKYGAFTPSLFGSEFFMGQMLKRLPESRICFLEGWNSNLYAANLQDSLYWAS 352
Db 692 SPYEVGFLKYGAFTPSLFGSEFFMGRLMRRIPPEPRICFLEAIVSNIFSLNLLDAWYDIT 751
Qy 353 EPSQFMDRWVRNQA-NLDKEQVPLL-----KIEB---PPSTAGRIAEFFTDLLTWPLA 402
Db 752 SSGESWQKHIDKTRSLKE--PLTTSQTSRLEASWLOQGT--LAQAFGLTGRPLH 807
Qy 403 QATHNFRGLHFHKDYFOHPHFSTWKAATLQPLNQLTSEPHCLLDVGYLINTSCPL 462
Db 808 QSPNPLQGLQLHODYCSHKDFSTWADYQDLSMPSQLTPKEPRCLVDAAYFINITSSPM 867
Qy 463 LQPTRDVLILSLDYNLHGAFQQLQGLGRFQEQGIPFPISPSPEQLQPRECHTSDPT 522
Db 868 FRPGRRLDILSFDYSLSAPFEALQOTELYCRARGLPFRVPEPSQDQHPRECHLFSDP 927
Qy 523 TCGAPAVLHP-----SSGVRTPEEAAAGVNLSSSDSPHYTKVTSQSDVD 571
Db 928 ACPEAPILLHPLVNNASFKDHSAPGVQSPAELOGGQVDTGATCTYLSNNITKEEDFE 987
Qy 572 KLLHLTHYVNCNNOELLEALROAVRRORR-QRRP 604
Db 988 LLRLSLDYNVQTSQAILQALRTALKHRTLEARP 1021
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RESULT 9

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US-10-467-248-1
; Sequence 1, Application US/10467248
; Publication No. US20040086905A1
; GENERAL INFORMATION:
; APPLICANT: DAS, Debopriya; YAO, Monique G.;
; APPLICANT: ARVIZU, Chandra S.; BAUGHN, Mariah R.;
; APPLICANT: LU, Yan; HAFALIA, April J.A.;
; APPLICANT: CHAWLA, Narinder K.; GRIFFIN, Jennifer A.;
; APPLICANT: LU, Dyung Aina M.; YUE, Henry;
; APPLICANT: DING, Li; ELLIOTT, Vicki S.;
; APPLICANT: FORSYTHE, Ian J.; RAMKUMAR, Jayalaxmi;
; APPLICANT: GANDHI, Ameena R.; ISON, Craig H.;
; APPLICANT: WARREN, Bridget A.; TANG, Y. Tom;
; APPLICANT: EMERLING, Brooke M.; HONCHELL, Cynthia D.;
; APPLICANT: LYNE, Michael; BARROSO, Ines
; TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
; FILE REFERENCE: PI-0358 USN
; CURRENT APPLICATION NUMBER: US/10/467,248
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03813
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,910
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; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/276,891
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/276,855
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/279,760
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/283,818
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/285,405
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 996
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7472774CD1
US-10-467-248-1

Query Match      38.4%; Score 1243.5; DB 16; Length 996;
Best Local Similarity 44.8%; Pred. No. 6.6e-109;
Matches 261; Conservative 86; Mismatches 187; Indels 49; Gaps 9;

QY 56 RDGSGIQQPPPLGKFRSCLS-----LPSSWDYRL-----RELAVRLGFGPCABEQ 101
Db 419 RKKGPIISQ-----LDCLSDGQVMTLPVGSYELHMKSTPCPETLDVRLGFSLCPAELE 472
QY 102 FLSSRKQVAAALRQALQDGLQDEIPVVAIMATGGIRAMTSLXGQLAGLKEGLD 161
Db 473 FLQKKVVVAKALKQVQLQEDLQEDVPLIATWATGGTRMSMTGCHLLGLQKLNLD 532
QY 162 CVSYITGASGTSWALANLYEDPEWSQKDLAPTELLKTQVTKNKLGLVAPLSQORQEL 221
Db 533 CASYIITGLSGATWMTATLYRDPDWSSKNLBPATFEARRHVVKDKLPFLFPDQLRKFOBEL 592
QY 222 ABRARLYGPCFTNLWALINEALLHDPHKLSDQREALSHGONPLPIYCALNTKQSL 281
Db 593 RORSQEGYRVTFTDFWGLLIETCLGDRNECKLSDQRAALS CGQNPPIYLTINVKDD-- 650
QY 282 TTFEGGWCFCFSPVEVGFPKYGAFIPSELFGSEFFMGKMLRPESRICLEGWSNLYA 341
Db 651 VSNQDVWFVFEFSPVEVGLQKYGAFIPSELFGSEFFMGKMLRKVRIPESSICVWMLGWSIFS 710
QY 342 ANLQDSLYWASEFSQFWRVNRQANLDKQVPLLKIEEPPSTAGRIAE----- 390
Db 711 LNLDDAWNLSHTSEFFHRTWREKVQ--DIEDEPIL--PEIPKCDANILETTVVIPIGWSLS 767
QY 391 -FTDILLTWPLAQATHNLFGLHFKDYFQHPHFSTWKTATLTDGLPNQLTSPSEPHCLL 449
Db 768 NSPREILTHRSFVSEFHNFLSGLQLHTNYLQNGQFSRWKQTVLVDGFPNQLTSEANHICLL 827
QY 450 DVGVLINTSCLPILOPTRDVLILSLDYNLHGAFQQLQLGRFCOEQIPPPISPSPEE 509
Db 828 DTAFFVNSYPPPLRPKADLIILHNYCAGSQTKPLQTCYEYCTVQNPFPKYE-LPDE 886
QY 510 QLOPRECHTSDPTCPGAPAVLHF-----SSGVRTPEAAAGEVNLSSSDSPY 558
Db 887 NENLKECVLMENPQEPDAPITVTFPLINDTPRKYKAPGVRSPEELEQGGQVDIYGKTPY 946
QY 559 HYTKVTSQEDVDKLLHLYTHVNCNNQEOLEALROAVORRQ 601
Db 947 ATKELTYTEATFDKLVKLSYNNILNNKDTLLQALRLAVEKKR 989

RESULT 10
US-10-380-873B-1
; Sequence 1, Application US/10380873B
; Publication No. US20040014089A1
; GENERAL INFORMATION:
; APPLICANT: Hiromasa MIYAJI, et al.

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; TITLE OF INVENTION: Polypeptide having phospholipase A2 activity
; FILE REFERENCE: 2139.34
; CURRENT APPLICATION NUMBER: US/10/380,873B
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: JP 00/146466
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: JP 01/284044
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-873B-1

Query Match      35.2%; Score 1139.5; DB 15; Length 849;
Best Local Similarity 41.8%; Pred. No. 4.4e-99;
Matches 250; Conservative 94; Mismatches 213; Indels 41; Gaps 9;

QY 43 MESLSVAQAG-----VQMRDLGS-----LQPPPLGFKFRFSCLSLPSWDYRLR----- 85
Db 250 MELLAAVQSGPSTELBAQTSKLGEGGILLSSDPLGQEEQCSVALGEGQEVVALSKMVKEMSS 309
QY 86 -ELAVRLGFGPCABEQAFLSRRKQVAAALRQALQDGLQDEDEIPVVAIMATGGIRAM 144
Db 310 GDLDLRLGFDLSGEGQEFLLDRRKQVVKALQVVLGLSEALDSQVVPVAVLGGSGGTRAM 369
QY 145 TSYGQLAGLKEGLDVCYSYITGASGTSWALANLYEDPEWSQKDLAPTELLKTQVTKN 204
Db 370 SSSYGLSLAGLQELGLDVTYLSGVSGSTWCISTLYRDPAWSQVALQSPITERAQVHVCCS 429
QY 205 KLGVLAPSQORQYRQELABEARLYGSCFTNLWALINEALLHDPHKLSDQREALSHG 264
Db 430 KMGALSTERLOYYTQELGVRSRSHSVSLDLMGLVLEYLLYEENPAKLSDDQEAVRQ 489
QY 265 QNPLPIYCALNTKQSLTTFEGGWCFCFSPVEVGFPKYGAFIPSELFGSEFFMGKMLR 324
Db 490 QNYPYITSVNR--TNLSGEDFAEWCEFTYEVGFPKYGAVVPELFGSELFGRLQLQ 548
QY 325 PESRICLEGWNLVYANLQDSLYWASEFSQFWRVNRQANL--DKEQVPLLKIEEPP-- 382
Db 549 PEPRICVLCQMGWSAFATSLDEIFLKTAGSGLSFLWYRGSVNITDDCQKP--QLHNPSR 605
QY 383 -----STAGRIAEFFTDLLTWPLAQATHNLFGLHFKDYFQHPHFSTWKTATLTDGLP 436
Db 607 LRTLITPQGPFSQAVLDIFTSRFTSAQSFNTRGLCLHKDYVAGREFVAKDTHPDAPF 666
QY 437 NQLTSPSEPHCLLDVGYLINTSCLPILOPTRDVLILSLDYNLHGAFQQLQLGRFCOEQ 496
Db 667 NQLTSPREDCILYVDGGAINSFPPLALLPQRAVDLILSFDYSLEAPEVFLKMKTEKYLDR 726
QY 497 GIPFPPTSPEBOLQPRECHTSDPTCPGAPAVLHF-----SSGV-RTPEEA 544
Db 727 GIPFPSTEVEGPEDEVEARECYLFAKEDRPSIVLHFFLNVNRTFRTHLAPGVERQTAEEK 786
QY 545 AAGEVNLSSDSPHYTKVTSQEDVDKLAHLHLYTHVNCNNQEOLEALROAVORROR 602
Db 787 AFGDFVINRPTPYGMNFTYEPQDFYRLVALSKYNNVNLNNVETLKCALQALDRHQAR 844

RESULT 11
US-10-380-873B-38
; Sequence 38, Application US/10380873B
; Publication No. US20040014089A1
; GENERAL INFORMATION:
; APPLICANT: Hiromasa MIYAJI, et al.
; TITLE OF INVENTION: Polypeptide having phospholipase A2 activity
; FILE REFERENCE: 2139.34
; CURRENT APPLICATION NUMBER: US/10/380,873B
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: JP 00/146466

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; PRIOR APPLICATION NUMBER: JP 01/284044
 ; PRIOR FILING DATE: 2001-05-16
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 38
 ; LENGTH: 853
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-380-873B-38

Query Match 35.2%; Score 1138; DB 15; Length 853;
 Best Local Similarity 42.4%; Pred. No. 6.2e-99;
 Matches 235; Conservative 102; Mismatches 189; Indels 28; Gaps 7;
 QY 74 LSLPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAALRQALQDGLQDEIPVVA 133
 Db VSLRMKADMSGDLRLGLFDLDCGEQFLDKRKQVASKALQRMVGLSEALHCDQVPVVA 354
 QY 134 IMATGGGIRAMTSLYQLAGLKLGLLDCVSYITGASGTWALANLYEDPEWSQKDLAGP 193
 Db VLGSGGGTTRAMTSLYGLAGLQBLGLLDAVTYLSGVSGSWCISTLYRDPSPSKALQGP 414
 QY 194 TELLKQVTKNKLGLVLAPSQLORYOELAEARLGYPCFTNLWALINEALLHDEPHDK 253
 Db 415 IKYASERVCSKLGMLSPKQFEYYSREKRAWESRHSMSFTDLWGLIIEYFLNQEENPAK 474
 QY 254 LSPQREALSHGONPLPIYCALNTKGSLTTFEGEWCFSPEYVGFPGKYGAFIPSELFGS 313
 Db 475 LSDQETVSGQGNPYPIYASINVH-KNISGDDFAEWCEFTPEYVGFPGKYGAYVTELF 533
 QY 314 EFPWGOLMKRLPESRSCFLEGINLSYANLQDLSYWASEPQFWRWVRNQANLDEQV 373
 Db 534 EFPWGLLHFWPEPRICYLQGMGSAFAASLYEFLKGLGLSLFLDWHRGVSFV-TDDW 592
 QY 374 PLIKIEEPPSTAGRI-----AEFFTDLTLTWPLAQATHNLRGLHFKDYFQHPHF-- 424
 Db 593 PKLRKQDPTLPTLPTMSSFSQAVLDIFTSITCAQTFNTRGLCMKYDYTKARDQFVV 652
 QY 425 --STWKATL---DGLPNQLTPSEPHCLLDVGYLINTCLPLQPTRDVLLSLDYL 479
 Db 653 SEDAMSHNYGVDPACPNQLTPMKDFSLVDGGFAINSPFPLVLPQRAVDLIVSFDYSL 712
 QY 480 HGAFOQLLGRCCQOGTFFPPIPSPEQLOPQRECHTFSDPTCGAPAVLHF----- 533
 Db 713 EGFEVLQVTEKYCRDRGIPFPRIEVDPKDSEDPRECYLFAEAEDPCSPVLHFLPLVNR 772
 QY 534 -----SSGV-RRTPPEAAAGEVNLSSDSPHYTKVTSQEDVDKLLHLTHYVNCNQE 587
 Db 773 FRTHLAPGVERQTAEBKAFGDFIINGPDTAYGMDFTEYEPKFDRLVTLRYNLNKKET 832
 QY 588 LLEALRQAVRRRQ 601
 Db 833 IRHALQALDRRRQ 846

RESULT 12
 US-10-380-873B-22
 ; Sequence 22, Application US/10380873B
 ; Publication No. US20040014089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiromasa MIYAJI, et al.
 ; TITLE OF INVENTION: Polypeptide having phospholipase A2 activity
 ; FILE REFERENCE: 2139.34
 ; CURRENT APPLICATION NUMBER: US/10/380,873B
 ; PRIOR FILING DATE: 2003-07-09
 ; PRIOR APPLICATION NUMBER: JP 00/146466
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: JP 01/284044
 ; PRIOR FILING DATE: 2001-05-16
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 22
 ; LENGTH: 854

; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-380-873B-22
 Query Match 34.8%; Score 1127; DB 15; Length 854;
 Best Local Similarity 42.6%; Pred. No. 7e-98;
 Matches 231; Conservative 100; Mismatches 183; Indels 28; Gaps 7;
 QY 86 ELAVRLGFGPCAEEQAFLSRRKQVVAALRQALQDGLQDEIPVVAIWATGGGIRAMT 145
 Db 308 DLDRLGLFDLDCGEQFLDKRKQVASKALQRMVGLSEALHCDQVPVAVVVGSGGTAMT 367
 QY 146 SLYGQLAGLKLGLLDCVSYITGASGTWALANLYEDPEWSQKDLAGTPELLTKTVTKN 205
 Db 368 SLYGSLAGLQELGLLDAVTYLSGVSGSWCISTLYRDPSPSKALQPIKYASERVCSK 427
 QY 206 LGVLAPSQLORYOELAEARLGYPCFTNLWALINEALLHDEPHDKLSDQREALSHGQ 265
 Db 428 IGMLSPKQFEYYSREKRAWESRHSMSFTDLWGLIIEYFLNQEENPAKLSDOQETVSQ 487
 QY 266 NPLPIYCALNTKGSLTTFEGEWCFSPEYVGFPGKYGAFIPSELFGSEFFMGOLMKRLP 325
 Db 488 NFYPIYASINVH-KNISGDIYFAEWCEFTPEYVGFPGKYGVVPTLFGSEFFMGRLHFWP 546
 QY 326 ESRICFLEGINLSYANLQDLSYWASEPQFWRWVRNQANLDEQVPLKIEEPPSTA 385
 Db 547 EPRICYLQGMGSAFAASLYEFLKGLGLSLFLDWHRGVSFV-TDDWPKLRQDPTRLP 605
 QY 386 GRI-----AEFFTDLTLTWPLAQATHNLRGLHFKDYFQHPHF-----STWKATL-- 432
 Db 606 TRLFTPMSSFSQAVLDIFTSITCAQTFNTRGLCMKYDYTKARDQFVWSEDAWHSNHYG 665
 QY 433 -DGLPNQLTPSEPHCLLDVGYLINTCLPLQPTRDVLLSLDYLNLHGAFQOLQLGR 491
 Db 666 PDACPNQLTPMKDFSLVDGGFAINSPFPLVLPQRAVDLIVSFDISLGSPFVLQVTEK 725
 QY 492 FQEQGIPFPPIPSPEQLOPQRECHTFSDPTCGAPAVLHF-----SSGV-RR 539
 Db 726 YCRDRGIPFPRIEVDPKDSEDPRECYLFAEAEDPCSPVLHFLPLVNRTRTHLAPGVERQ 785
 QY 540 TPEAAAGEVNLSSDSPHYTKVTSQEDVDKLLHLTHYVNCNQEOLLEALRQAVRR 599
 Db 786 TAEBKAFGDFIINGPDTAYGMDFTEYEPKFDRLVTLRYNLNKKETIRHALQALDRR 845
 QY 600 RQ 601
 Db 846 RQ 847

RESULT 13
 US-10-332-426-3
 ; Sequence 3, Application US/10332426
 ; Publication No. US20040029136A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom;
 ; APPLICANT: AZIMZAI, Yalda; DAS, Debopriya;
 ; APPLICANT: THORNTON, Michael; LU, Dyung Aina M.;
 ; APPLICANT: TRIBOULET, Catherine M.; YUE, Henry;
 ; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
 ; APPLICANT: KHAN, Farrah A.; LU, Yan;
 ; APPLICANT: YAO, Monique G.; HAFALIA, April J. A.;
 ; APPLICANT: BELLITT, Vicki S.; ARVIZU, Chandra S.;
 ; APPLICANT: IAL, Preeti; RAMKUMAR, Jayalaxmi;
 ; APPLICANT: NGUYEN, Dannie B.; BAUGHN, Mariah R.
 ; TITLE OF INVENTION: LIPID METABOLISM MOLECULES
 ; FILE REFERENCE: PI-0152 USN
 ; CURRENT APPLICATION NUMBER: US/10/332,426
 ; CURRENT FILING DATE: 2003-01-06
 ; PRIOR APPLICATION NUMBER: US 60/216,803
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 60/216,801
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 60/218,233


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; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/220,046
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US 60/220,739
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/222,824
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. US20040029136A1 1281946CDI
US-10-332-426-3

Query Match      34.4%; Score 1112; DB 12; Length 848;
Best Local Similarity 41.2%; Pred. No. 1.9e-96;
Matches 247; Conservative 97; Mismatches 211; Indels 44; Gaps 11;

QY 43 MSLSLVAQAG-----VQWRDLGS-----IQPPLGKRFSC-----LSLPSSWDYR 83
Db 250 MELLAAVQSGPSAELEAQTSLGEGGILLSSPLG-QEEQCSVALGEGEGVALSMTVEMS 308
QY 84 LRELAVRLGFGCAEBAEQAFSLRKKQVVAALRQALQOLDGLODEIPVVAIMATGGIRA 143
Db 309 SGBLDURLGLDSDGQEFLLRRKQVVKALQVLGLSEALDSGQVPVAVLGGGGTGA 368
QY 144 MTSLYQLAGLGLGLDCVSYITGASGSTWALANLYDEPWSQKDLAGTTELLKTQVTK 203
Db 369 MSSLYSGLAGLBGLLDVTVYLSVSGSTWCTISTLYRDPANQVALQGPRAQVHVS 428
QY 204 NKLGVLAPSOQYRQELAEARLGPSPCTNLMALINEALLHDEPHDKLSQREALSH 263
Db 429 SKMGALSTERLQYVQELGVRERSGHSVSLDLWGLLVEYLLYQEEENPAKLSQQAQVR 488
QY 264 GNPPLIYCALNTKQSLITFECEGCEFSPEYVGPYKCAFIPSELFGESEFPGQLMKR 323
Db 489 GQNPYPIYTSVNVYR-TNLGSEDA-WCEFTPYKVPKYGAYVTELFGESEFPMGLLQL 546
QY 324 LPESRICFLEGIWSNLYAANLQDSLYWASEPQFWRWVNRQANL-DKEQVPLLKTEEPP 382
Db 547 QEPERICYLQGMWSAFATSLDIFLKTAGSGLSFLWYRGSVNITDDCQX--QLHNPS 604
QY 383 -----STAGRIARFTDLLWRPLAQATHNRLGLHFHKOYFQHPHFSTWKTATLDGL 435
Db 605 RLKRLTLTPQGPFSQAVLDIFTSRFTSAQSFNFTRGILCLHKDYVAGREFVAKDTHPDAF 664
QY 436 PNOLTFSEPHCLLDVGYLINTSCLPLQPTQTRVDLTLSDYNLHGAFOQLLGRPCOE 495
Db 665 PNOLTPMRDCLYLDVGGAFFALNSFPFALLPQRAVDLTLSPDYSLEAPFEVLKMTKXYCLD 724
QY 496 QGIPFPPIPSPEQLOPQPRECHTFSDPTCPGAPAVLHF-----SSGV-RRTPEE 543
Db 725 RGIPFSIEVGPEDVEARECYLFAKAEADPRSPVLVHFLPVNRTFRTHLAPGVERTASE 784
QY 544 AAGEVNLSSDSPHYHVKTYTGOEDVDKLLHLYTHVNCNNQOLLEALRQAVORRRQ 602
Db 785 KAFGDFVINRPTPYGMNFTYEPQDFYRLVALSRVNLNNVETLKCALKALDRLDQAR 843

RESULT 14
US-10-211-462-50
; Sequence 50, Application US/10211462
; Publication No. US20040033495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
```

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; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 50
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-50

Query Match      19.1%; Score 619; DB 12; Length 749;
Best Local Similarity 27.1%; Pred. No. 1.9e-49;
Matches 174; Conservative 125; Mismatches 238; Indels 106; Gaps 22;

QY 44 ESLSVAQAGVQWRDLGSLQPPPLGKRFSCLSIPSSWDYRLRELA---VRLGFGCAEE 99
Db 100 ETLGATFTVSSMKVGEKEVEFIFNQVTEMVLEMS-----LEVSCPDRLRSMALCDOE 154
QY 100 QAFLSRRKQVAAALRQAL---QLDGLQEDHPIPVVAIMATGGIRAMTSLYQLAGLKE 156
Db 155 KTFRQQRKEHIRESMKLLGKXNSEGLHSARDVPVVAIILGSGGPRAMVFGSGVMKALYE 214
QY 157 LGLLDCVSYITGASGSTWALANLYDEPWSQKDLAGTTEL---LKTQVTKNLGLVLAPSQ 213
Db 215 SGILDCAVTVAGLSGTWTMYSTLYSHPDPEK---GPERINEELMKNVSHNPLLLTPOK 271
QY 214 LQRYRELAERARLGPSPCTNLMW-LINEALLHDEPHDKLSQREALSHGQNPLPIYC 272
Db 272 VKRYVESLWKXSSGGQPTFTDIFGLMIGETLIHNRMT-TLSSLKEKNTACQPLPLFT 330
QY 273 ALMTKQQSITTFEFGWCCEFSPEYVGPYKCAFIPSELFGESEFPMGLMKRLPESRICFL 332
Db 331 CLHVK-PDVSSELMFADWVEFSPEYIGMAKYGTFTMAPDLFGSKFFMGTVVKKYEENPLHFL 389
QY 333 EGIWSNLYA-----ANLQDSLYWASEPQFWRWVNRQANLDEQVPLL 376
Db 390 MGVMGSAFSLFNRLVGLVSGSQRSGSTMBEEL-----ENITTKHIVSNDSSDSD--- 439
QY 377 KTEEPSTAGRIA--EFFTD-----LLTWRPLAQATHNRLGLHFH 415
Db 440 ESHEPKGTENEDAGSYQSDNQASWTHRMIMALVSDALFNTEGRAGKXVHFMGLNLN 499
QY 416 KOYFQHP--HFSTWKTATLDGL-----PNQ-----LTPSEPHCLLDVGYLINTSCL 460
Db 500 TSYPLSPLSDFATQDSFDDDELDAADVADPEFERIYEPDLVKSXKTHVVDVSGLTFLNLYP 559
QY 461 PLLOPTRDVLTLSDYNLHGA-----FOQLLGRFCOEQIGIPFPPIPSPEQLOPRE 515
Db 560 LILRQGRVDLILSIFDSARPDSPPPELLAEKXAKMKNKLPFPKIDPFYVDFREGLKE 619
QY 516 CHTFSDPTCP---GAPAVLHF-----SSGV-RRTPEEAAAGEVNL-SSSDSPY 558
Db 620 CVYFK-PKNPDMKEKOCPTIHFVLANINFRKYKAPGVPRETEEEKIADPIDFDDPESPF 678
QY 559 HYTKVTYSQEDVDKLLHLYTHVNCNNQOLLEALRQAVORRRQ 601
Db 679 STENFOYPNQAFKRLHDLMHFNTLNNIDVIDVKEAMVESIEYRRQ 721

RESULT 15
US-10-157-898-2
; Sequence 2, Application US/10157898
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; Publication No. US20030225011A1
; GENERAL INFORMATION:
; APPLICANT: DAVID, Samuel
; TITLE OF INVENTION: PHOSPHOLIPASE A2 EXPRESSION AND ACTIVITY AND USE THEREOF FOR DIAGNOSIS AND TREATMENT OF NEURAL INFLAMMATORY DISEASE
; TITLE OF INVENTION: PHOSPHOLIPASE A2 EXPRESSION AND ACTIVITY AND USE THEREOF FOR DIAGNOSIS AND TREATMENT OF NEURAL INFLAMMATORY DISEASE
; TITLE OF INVENTION: PHOSPHOLIPASE A2 EXPRESSION AND ACTIVITY AND USE THEREOF FOR DIAGNOSIS AND TREATMENT OF NEURAL INFLAMMATORY DISEASE
; FILE REFERENCE: 85827-36
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent version 3.1
; SEQ ID NO 2
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-898-2

Query Match      19.1%; Score 619; DB 12; Length 749;
Best Local Similarity 27.1%; Pred. No. 1.9e-49;
Matches 174; Conservative 125; Mismatches 238; Indels 106; Gaps 22;

QY 44 ESLSVAQGVQVRDLGSLQPPPLGKRFKFSCLSLPSSWDYRLRLRLA-----VRLGFGPCABE 99
Db 100 ETLGATATFTVSSMKVGEKVPFIFNQVTEMVLEMS-----DEVSCPDLRFSMALCDQE 154

QY 100 QAPLSRRKQWAAALRQAL---QLDGDLOEDEIPVVAIMATGGGIRAMTSLYGOLAGLKE 156
Db 155 KTFRQQRKEHIRESMKLLGPKNSEGLHSARDVPVVAIIIGSGGFRAMVGFSGVMKALYE 214

QY 157 LGLLDCVSYITGASGTWALANIYEDPEWSQKDLAGPTL---LKTQVTNKNLGLVLAPSQ 213
Db 215 SGILDCATYVAGLSGSTMWSTLYSHPDPEK---GPEEINBELMKNVSHNPLLLTPOK 271

QY 214 LQRYQELAEARLGPSCFTNLWA--LINEALLHDEPHDKLSQDREALSHGQNPPIYC 272
Db 272 VRYVESLWKKSSGQVFTTDFIGMLIGETLIHNMNT--TLSSLKEKVTACQPLPLFT 330

QY 273 ALNTKQSLLTFEFGWCFCFSYEVGPKYGAIPSELFSGSFFFMQMLMKRLPESRICFL 332
Db 331 CLHVK--PDVSELMFADWVFSPEIGMAKYGTFMADPLFGSKFFMGTVVKYEEENPLHFL 389

QY 333 EGIWSNLYA-----ANQDSLYWASEPSQFWDNRWVRNQANLDKEQVPLL 376
Db 390 MGWVGSFAFILFNRLVGVSGSQSRGSTMEEEL-----ENITTKHIVSNDSDSD-- 439

QY 377 KIEEPSTAGRIA--BFTD-----LLTWRLPAQATHNPLRGLHFL 415
Db 440 ESHEPKGTENEDAGSDYQSDNQASWIHRMIMALVSDSALFNTREGRAGKVNHPMLGILNL 499

QY 416 KDYFQHP--HFSTWKAATLIDL-----PNQ-----LTPSEPHLCLLDVGYLINTSCL 460
Db 500 TSYPLSPLSDFATQDSFDDDELDAADVADFEFRIYEPDLVKSKKIHVVDSGLTFNLPPY 559

QY 461 PLLQPTRVDLILSLDYNLHGA-----FOQLLGRFCOEQIGIPPPPIPSPEEQLOPRE 515
Db 560 LILRQGRVDLIIISDFSRPSDSSPPFKELLIAEKWAKNKLPPPKIDPIYVDFREGLKE 619

QY 516 CHTFSDPTCP---GAPAVLHF-----SSGV--RRTPEEAAAAGVNL--SSSDSPY 558
Db 620 CIVFK--PKNPDMEKDCPTIIHFVLANINFKRYKAPGVPRETEEEKIADFIDDDPESPF 678

QY 559 HYTKVTSQEDVDKLLHLTHYVNNQEQQLLEALRQAVORRQ 601
Db 679 STFNFOYPNQAFKRLHDLMHFNTLNNIDVIKEAMVESIEYRQ 721

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Search completed: October 5, 2004, 19:41:16
Job time : 141.133 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 19:21:45 ; Search time 41.14 Seconds
(without alignments)
1414.581 Million cell updates/sec

Title: US-09-830-321A-2
Perfect score: 3235
Sequence: 1 MIFVLSPTLALCLERVASH.....EQLEALRQAVQRQRPH 605

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	619	19.1	749	1 A39329	phospholipase A2 (
2	602	18.6	749	1 B39898	phospholipase A2 (
3	596	18.4	748	1 I50699	cytosolic phosphol
4	572	17.7	741	2 B54908	phospholipase A2 c
5	498.5	15.4	541	2 T13162	cytosolic phosphol
6	198	6.1	627	4 A40201	artifact-warning s
7	193.5	6.0	613	4 C40201	artifact-warning s
8	186	5.7	673	2 T50281	probable lysophosp
9	184	5.7	686	2 S66693	hypothetical prote
10	177	5.5	612	2 S29318	lysophospholipase
11	170	5.3	46	2 I54375	gene NF2 protein -
12	162	5.0	664	2 S53037	PLB1 protein - yea
13	160	4.9	39	2 I54374	gene NF2 protein -
14	159.5	4.9	623	2 T40891	probable lysophosp
15	159	4.9	624	2 T38006	probable lysophosp
16	158	4.9	53	2 A42442	integrin beta-1 ch
17	154	4.8	754	2 T18238	lysophospholipase
18	151	4.7	613	2 T38007	probable lysophosp
19	140	4.3	644	2 T37800	probable lysophosp
20	136	4.2	706	2 S53035	probable lysophosp
21	124	3.8	100	2 A46010	X-linked retinopat
22	122.5	3.8	673	4 F40201	artifact-warning s
23	122	3.8	536	2 S62110	lysophospholipase
24	118.5	3.7	1749	2 S75071	hypothetical prote
25	105	3.2	431	2 JC4805	core protein F - p
26	103.5	3.2	597	4 E40201	artifact-warning s
27	103	3.2	432	2 T10894	neuronal pentraxin
28	101.5	3.1	946	2 I38100	rho-GTPase-activat
29	101	3.1	372	2 T25621	hypothetical prote

30	101	3.1	1188	2 D86311	protein Fli3.20 [i
31	100.5	3.1	1461	2 B70588	probable polyketid
32	100	3.1	252	2 B82181	oxidoreductase, sh
33	99.5	3.1	1026	2 G81751	exodeoxyribonuclea
34	99.5	3.1	2611	2 T14591	actinomycin synthe
35	99	3.1	690	2 D75487	v-type ATP synthe
36	99	3.1	4687	1 A39638	plectin - rat
37	98.5	3.0	440	2 A26359	decay-accelerating
38	97	3.0	852	1 GNUGA	poi polyprotein -
39	96	3.0	361	2 AD1079	glucosamine-fructo
40	96	3.0	624	2 T39102	hypothetical prote
41	96	3.0	781	2 S37032	gene LL5 protein -
42	96	3.0	873	1 TVFVF	protein-tyrosine k
43	96	3.0	883	2 A49733	[heparan sulfate] -
44	95.5	3.0	569	2 C86934	probable membrane
45	95.5	3.0	613	2 AC2962	hypothetical prote

ALIGNMENTS

RESULT 1

A39329 phospholipase A2 (EC 3.1.1.4), cytosolic - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 20-Apr-2000
R;Sharp, J.D.; White, D.L.; Chiou, X.G.; Goodson, T.; Gamboa, G.C.; McClure, D.; Burgett, J. Biol. Chem. 266, 14850-14853, 1991
A;Title: Molecular cloning and expression of human Ca(2+)-sensitive cytosolic phospholipase A2
A;Reference number: A39329, MUID:91331987; PMID:1869522
A;Accession: A39329
A;Molecule type: mRNA
A;Residues: 1-749 <SHA>
A;Cross-references: GB:M68874; NID:gl90003; PIDN:AAA60105.1; PID:gl90004
R;Clark, J.D.; Lin, L.L.; Kriz, R.W.; Ramesha, C.S.; Sultzman, L.A.; Lin, A.V.; Milona, R. Cell 65, 1043-1051, 1991
A;Title: A novel arachidonic acid-selective cytosolic PLA-2 contains a Ca(2+)-dependent t
A;Reference number: A39898; MUID:91256305; PMID:1904318
A;Accession: A39898
A;Molecule type: mRNA
A;Residues: 1-749 <CLA>
A;Cross-references: GB:M72393; NID:gl90006; PIDN:AAB00789.1; PID:gl90007
A;Note: part of this sequence was confirmed by protein sequencing
R;Li, B.; Copp, L.; Castelhan, A.L.; Feng, R.; Stahl, M.; Yuan, Z.; Krantz, A. Biochemistry 33, 8594-8603, 1994
A;Title: Inactivation of a cytosolic phospholipase A-2 by thiol-modifying reagents: cyste
A;Reference number: A54198; MUID:94304876; PMID:8031794
A;Accession: A54198
A;Molecule type: protein
A;Residues: 319-338; X', 340-345; X', 347-358 <LJA>
A;Note: modification of preferred modification site Cys-324 abolished enzymatic activity
R;Gordon, R.D.; Leighton, I.A.; Campbell, D.G.; Cohen, P.; Creaney, A.; Wilton, D.C.; Mas Eur. J. Biochem. 238, 690-697, 1996
A;Title: Cloning and expression of cytosolic phospholipase A(2) (cPLA(2)) and a natural results in an increase in specific activity.
A;Reference number: S68897; MUID:96300233; PMID:8706669
A;Accession: S68898
A;Molecule type: protein
A;Residues: 497-507 <GOR>
C;Comment: This cytosolic phospholipase A2 translocates to membrane vesicles in response
C;Genetics:
A;Gene: GDB:PLA2C4A; PLA2G4
A;Cross-references: GDB:134687; OMIM:600522
A;Map position: 1q25-1q25
C;Superfamily: cytosolic phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; cytosol; inflammation; phosphoprotein F;505/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 19.1%; Score 619; DB 1; Length 749;
Best Local Similarity 27.1%; Pred. No. 1.1e-39;
Matches 174; Conservative 125; Mismatches 238; Indels 106; Gaps 22;

44 ELSVAQAGVQWRDLGSLQPPPLGFRFSCLSGLPSSWDYRLRELA-----VRLGFGPCABE 99
100 ETLGTATFTVSSMKVGEKEVFFINQVTEMVLEMS-----LEVCSCPDLRFSMALCDQE 154
100 QAFLSRRKQVAAALRQAL---QLDGLQDEIPVVAIMATGGIRAMTSLYQLAGLKE 156
155 KTFQORKEBHRESMKKLLGPNKNSGLHSARDVPVVAILGSGGFRAMVFGSGVMKALYE 214
157 LGLDCVSVITCAGSGTWALANLYDEPWSQKDLAGPTL---LKTQVTKNKLGLVAPSQ 213
215 SGILDCATYVAGLSGSTWMTSLYSHDPPEK---GPEINBELMKNVSHNLLLTPOK 271
214 LQRYQELAEARLGPSCFTNLWA-LINEALLHDEPHDKLSDOREALSHGQNPLPIYC 272
272 VKRYVESLWKKSSGQPVFTDFGLMIGETLIHNRMTI-TLSSLKEKVTACQPLPLFT 330
273 ALNTKGQSLTTFEGEWCBSFSEYVGFPPKYGAFIPSELFGSFFFMQMLKRLPESRICPL 332
331 CLHVK-PDVSELMFADWVEFSYVEIGMAKYGTFMADPLFGSKFFMGTVVVKYEENPLHFL 389
333 EGIMSNLYA-----ANLQDSLYWASEPQFQWDRWRVNRQANLDKEQVPLL 376
390 MGWGSASFILNRVLGVSGSQRSGSTMBEEL-----ENITTKHTVSNDSDD----- 439
377 KTEEPPESTAGRIA--EFFTD-----LLTWRLPAQAATHNRLGLHFF 415
440 ESHEPKGTENEDAGSDYQSDNQASWTHRMIMALVSDALFNTRREGRAGKVNFMGLNLN 499
416 KQYFQHP--HFSTWKATTLDEL-----LTPSEPHCLLDVGYLINTSCL 460
500 TGYPLSPLSDFATQSDFDDELDAVADPEFERIYEPLDVKSKKHIVVDVSGLTFNLXP 559
461 PLLQPRDVLILSDYNLHGA-----FOQLQLGRFCQEQGPFPPIPSPEQQLQPRE 515
560 LILRPOGVDLIISDFSARPSDSSPPFKELLAEKWKNNKLPFPKIDPVYDFRGLKE 619
516 CHTFSDPTCP---GAPAVLHF-----SSGV-RTPEEAAAGEVNL-SSSDSPY 558
620 CYVFK-PKPNDEKOCPTIIHFVLANINFRKYKAPGVPRETEBEKEIAFDIDDDPESP 678
559 HTYKVTYSQEDVKLLHLYNNVNCNQEQLEALRQAVQRRQ 601
679 STNFQYPNQAFKRLHLMHENTLNNIDVKEAMVESIEYRRQ 721
RESULT 2
B39898
phospholipase A2 (EC 3.1.1.4), cytosolic - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: B39898
R;Clark, J.D.; Lin, L.L.; Kriz, R.W.; Ramesha, C.S.; Sultzman, L.A.; Lin, A.V.; Milona,
Cell 65, 1043-1051, 1991
A;Title: A novel arachidonic acid-selective cytosolic PLA-2 contains a Ca(2+)-dependent
A;Reference number: A39898; MUID:91256305; PMID:1904318
A;Accession: B39898
A;Molecule type: mRNA
A;Residues: 1-749 <CLA>
A;Cross-references: GB:M72394
C;Comment: This cytosolic phospholipase A2 translocates to membrane vesicles in response
C;Superfamily: cytosolic phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; cytosol; inflammation
Query Match 18.6%; Score 602; DB 1; Length 749;
Best Local Similarity 27.1%; Pred. No. 2.3e-38;
Matches 172; Conservative 126; Mismatches 247; Indels 90; Gaps 21;
44 ELSVAQAGVQWRDLGSLQPPPLGFRFSCLSGLPSSWDYRLRELA-----VRLGFGPCABE 99
100 ETLGTATFTVSSMKVGEKEVFFINQVTEMVLEMS-----LEVCSCPDLRFSMALCDQE 154
100 QAFLSRRKQVAAALRQAL---QLDGLQDEIPVVAIMATGGIRAMTSLYQLAGLKE 156

155 KTFQORKEBHRESMKKLLGPNKNSGLHSARDVPVVAILGSGGFRAMVFGSGVMKALYE 214
157 LGLDCVSVITCAGSGTWALANLYDEPWSQKDLAGPTL---LKTQVTKNKLGLVAPSQ 213
215 SGILDCATYVAGLSGSTWMTSLYSHDPPEK---GPEINBELMKNVSHNLLLTPOK 271
214 LQRYQELAEARLGPSCFTNLWA-LINEALLHDEPHDKLSDOREALSHGQNPLPIYC 272
272 VKRYVESLWKKSSGQPVFTDFGLMIGETLIQNR-MSMTLSLKEKVNAAARCPPLFT 330
273 ALNTKGQSLTTFEGEWCBSFSEYVGFPPKYGAFIPSELFGSFFFMQMLKRLPESRICPL 332
331 CLHVK-PDVSELMFADWVEFSYVEIGMAKYGTFMADPLFGSKFFMGTVVVKYEENPLHFL 389
333 EGIMSNLYA-----ANLQDSL-----YWASEPQFQWDRWRVNRQANLDK 370
390 MGWGSASFILNRVLGVSGSQRSGSTMBEEL---ENITTKHTVSNDSDD---DEAOGPKGTEN 449
371 EQVPLLKITEPEPSTAGRIABFFDLDLTLWRPL-----AQATHNRLGLHFFHFDYFQHP- 422
450 EEAE--KEYQSDNQASWTHRMIMALVSDALFNTRREGRAGKVNFMGLNLNTSYLSPL 507
423 -HFSTWKATTLDEL-----PNO-----LTPSEPHCLLDVGYLINTSCLPLQPTD 468
508 RDFSQSDSDDELDAVADPEFERIYEPLDVKSKKHIVVDVSGLTFNLPIYLILRPOG 567
469 VLLILSDYNLHGA-----FOQLQLGRFCQEQGPFPPIPSPEBQLQPRECHTSDPT 523
568 VLLIISDFSARPSDSSPPFKELLAEKWKNNKLPFPKIDPVYDFRGLKECYVFK-PK 626
524 CP---GAPAVLHF-----SSGV-RTPEEAAAGEVNL-SSSDSPHYTKVTYS 566
627 NPDVEKDCPTIIHFVLANINFRKYKAPGVRLTEKEKEIAEDFIDDPESPSTFNFQYP 686
567 QEDVDKLLHLYNNVNCNQEQLEALRQAVQRRQ 601
687 NOAFKRLHLMYFNTLNNIDVKEAIVESIEYRRQ 721
RESULT 3
I50699
cytosolic phospholipase A2 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I50699
R;Nalefski, E.A.; Sultzman, L.A.; Martin, D.M.; Kriz, R.W.; Towler, P.S.; Knopf, J.L.; C
J. Biol. Chem. 269, 18239-18249, 1994
A;Title: Delineation of two functionally distinct domains of cytosolic phospholipase A2
A;Reference number: A54908; MUID:94299545; PMID:8027085
A;Accession: I50699
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-748 <NAL>
A;Cross-references: EMBL:U10329; NID:9508624; PIDN:AAA53228.1; PID:9508625
C;Superfamily: cytosolic phospholipase A2
C;Keywords: cytosol
Query Match 18.4%; Score 596; DB 1; Length 748;
Best Local Similarity 25.9%; Pred. No. 6.8e-38;
Matches 166; Conservative 129; Mismatches 245; Indels 100; Gaps 20;
44 ELSVAQAGVQWRDLGSLQPPPLGFRFSCLSGLPSSWDYRLRELA---VRLGFGPCABE 103
100 ETLGMATFTPISSLKLGKEKQVLTNNVTMTLELSLEV-CGSTDLRFSMALCDEBKFR 158
104 SRRKQVVAALRQALQDGD---LQDEIPVVAIMATGGIRAMTSLYQLAGLKEGLL 160
159 QQRKDMIMOSMKSFLEGENSKNLTTRDRVPVIAVLGSGGFRAMVFGAGVWKALYESGVL 218
161 DCVSYITGASGSGTWALANLYDEPWSQKDLAGPTL---LKTQVTKNKLGLVAPSQ 217
219 DCATYIAGLSGSTWMTSLYSHDPPEK---GPKINQELMNSVSHNLLLTPOKVKRY 275

Db 222 NYNDLRKEIDQKHAGFDCSLTDLW-----SRKLVDAERGGPGITYSSMRN 272
QY 261 ---LSHQONPLPIYCA-----LNTKQSLTTFEGCEWCEFSPEYGVGPKYCAFI 306
Db 273 QSWFQNDADYPIPIIVADSRLEEBETAIPANTSIEFFTAIEFGTW-----DNGIK---AFI 323
QY 307 PSELFGSEFFMGQMKRLPESRIC-----FLEGIWSNLYAANLQDSLYWASEPQWF 358
Db 324 PMEYVGT-----HLLDGVDPDKSCIHNVDNAGFWMGTSATLFSFLD-----W 367
QY 359 DRWRNQNANLQEQVPLLKIEEPPSTAGRIABEFTDLLTWRLPAAQATHNFLRGLHFHKO- 417
Db 368 NENVKKN-----DITYDIL-----HAILEDLSKHQDD 394
QY 418 --VFQHPH--FSTWKATTLQGLNQLTPSRPH--LCLLDVGY-LINTSCLPILQPTDQVD 470
Db 395 IAPYNPYQNTYTSNVNAP-----EPYTDILVDGGEDRENIPMLPLHPQRFVD 447
QY 471 LILSLD--YNLHGAFQOLQLGRFCQGIFFPPIPSPEEQLPQRECHTFSD-----PTC 524
Db 448 VFAIDSTYN-----DPYGMPLGSSIVATYERVVTFNANKSVDRVGFPIY 492
QY 525 PGAPAVLHFSGVGRT-----PREAAGEVNLSSDSP-----YHYTKVTYSQE 568
Db 493 PDENTIISLGLNTRPTFFGDCGNNTAGNHVDVNDNTPPLLVYFPNYPWTYYSNISFTMS 552
QY 569 DVKLLHLTHYVVC-----NNQQLLEALRQA-VORRRQR 603
Db 553 MDDKMANGILENFMSTTQNNESFAVCLACAIQRLSRK 593

RESULT 9
S66693
hypotheical protein YOL011w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypotheical protein G2349
C/Species: Saccharomyces cerevisiae
C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C/Accession: S66693
R/Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A/Reference number: S66685
A/Accession: S66693
A/Molecule type: DNA
A/Residues: 1-686 <HUG>
A/Cross-references: EMBL:Z74753; NID:g1419780; PIDN:CAA99010.1; PID:g1419781; GSPDB:GN00
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:PLB3; MIPS:YOL011w
A/Cross-references: SGD:S0005371
A/Map position: 15L
C/Superfamily: yeast lysophospholipase

Query Match 5.7%; Score 184; DB 2; Length 686;
Best Local Similarity 21.0%; Pred. No. 4.7e-06;
Matches 129; Conservative 80; Mismatches 192; Indels 214; Gaps 31;
QY 99 EQAFLRRKQVAAALRQAL-----QLDGLQDEIPVVAIMATGGGIRA 143
Db 57 ESNWLEKRNKVTVALKDFLTRATNPFSDSESVLSKLFDNDSNENUPKIAVAVSGGYRS 116
QY 144 MTSLYGQLAGLKE-----GLLDCVSYITGASGSTWALANL----- 179
Db 117 MLTGAGVLAAMNRTGAYEHLGLLQSTLYLSGASGNNWLVGTLALNNTWSVQDILNN 176
QY 180 --YEDPEWSKD--LAGPTLLKTVQTKNL-GVLAPOLOQRYRELAE---RAELGYP 230
Db 177 MQNDDSIWDLSDISVTPGGINIFKTAQRWDHISNAVESKQADYNTSLADIWGRA-LAY- 234
QY 231 SCPTNLWALINE-----ALLHDEPHDKLSQREALSHGQNPPLIYCA----LNTKQ 279
Db 235 ----NFFPSLNRRGIGLWTSIRDFP-----VFQNAEMFPFPISVADGRYPGTKVI 280
QY 280 SLTTFEGWCEFSPEYVGF--PKYGAFIPSELFSGEFFMGQLMKR-----LPESRICFLE 333

Db 281 NINATVF-----ENPPFMGSGWDFSLNSFANVKYLGTVNSGVPLERKCTAGFNAGFIM 336
QY 334 GIWSNLYAANLQDSLYWASEPQWFDRWRNQNANLQEQVPLLKIEEP--PSTAGRIA-- 389
Db 337 GTSSTLF-----NQF-----LLRINSTHLPSPFITRLARH 365
QY 390 -----EFFTDLTLTWRLPAAQATHNFLRGLHFHKOYFOHPHFWKATILDLGNLQPTSE 443
Db 366 FLKDLSDQDFNDIAVYSPNPFKTKFL-----DSDY-----SIYDSD 403
QY 444 PHCLLDVGY-LINTSCLPILQPTDQVDLILSLDYN-----LHGAFQOLQL 489
Db 404 -SFLVDGGEDDENVPVPLIQRVDIIFAVNSADMELAMPDGSLSLVHVERQFVKQ 462
QY 490 GRFCQGIFFPPIPSPEEQLPQRECHTF-----SDPTCPGA-----PAVL 531
Db 463 G-----QGMSPYVVP-----DTNTEVNLGLNKKPTFFGCDANNTDLQVIPPVV 507
QY 532 HFSSGVRRTPEEAAGEVNLSSDSPHYHYTKVTYSQED-----VDKLLHLTHYVNCNQE 587
Db 508 YLPN-----AEYSPNSQSAF-----KLSYSESQRSMIQNGFEIATRNNTDDE 553
QY 588 LLEALRQAVORRRQR 602
Db 554 FMGCVGCAIIRKQ 568

RESULT 10
S29318
lysophospholipase (EC 3.1.1.5) precursor [validated] - Penicillium notatum (fragment)
C/Species: Penicillium notatum
C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 19-Jan-2001
C/Accession: S29318; S39881; S22045
R/Masuda, N.; Kitamura, N.; Saito, K.
Eur. J. Biochem. 202, 783-787, 1991
A/Title: Primary structure of protein moiety of Penicillium notatum phospholipase B deduc
A/Reference number: S29318; MUID:92111525; PMID:1722456
A/Accession: S29318
A/Molecule type: mRNA
A/Residues: 1-612 <MAL>
A/Cross-references: EMBL:X60348; NID:g3183; PIDN:CAA42906.1; PID:g3184
A/Accession: S39881
A/Molecule type: protein
A/Residues: 10-20;185-199 <MA2>
C/Superfamily: yeast lysophospholipase
C/Keywords: carboxylic ester hydrolase; glycoprotein
F/1-9/Domain: signal sequence (fragment) #status predicted <SIG>
F/10-612/Product: lysophospholipase #status experimental <MAT>
F/41,81,116,223,267,306,335,427,440,446,477,498,536,532,567,571/Binding site: carbohydrat

Query Match 5.5%; Score 177; DB 2; Length 612;
Best Local Similarity 21.3%; Pred. No. 1.4e-05;
Matches 108; Conservative 60; Mismatches 162; Indels 178; Gaps 23;
QY 51 AGVWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELAVRLGFGPCAEQAFLSRRKQVV 110
Db 5 AGVQ-----RALFNAPDGY-----VPTSVSPASRPTVRSAAKLSTNETSWLEVRGKT 53
QY 111 AALRQ-----ALQLDGLD-QEDEIPVVAIMATGGIRAMTSLYGLQAGLKE 157
Db 54 LSAKLDFFGHVKGVDYDVGAYLDKXSGNSSSLPNIGIAVSGGWRALMNGAGAVKAFDSR 113
QY 158 -----GLLDCVSYITGASGSTWALANLY----- 180
Db 114 TDNATATGHLGILLQATVISGLSGSWLLGSIVINNFTVDKLTQTHEAGSVWQFNSII 173
QY 181 EDPEWSKDLAGTELLKTVQTKNLGVLAPOLOQRYRELAE----RAELGYPSCFTNL 236
Db 174 EGED-----AGTIQLLDS-----AGYYKDLADAVDGKKAGGDTTLTDI 212
QY 237 WALINEALLHDSPHD-----HKLSQREALSHGQNPPLIYCALNTK-----GQSLTTF 284

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Db 213 WGRALSYQMFNASNGSLSYTWSSIAITPE-FQDGYPMFPVAVDGRNPGELVIGSNSTVY 271
QY 285 EGEWCERSPYEVGPKYCAPISELFGSEFFMGQMKLPESRIC-----FLEGIM 336
Db 272 EFNPM-EFTFD---PTIFGVPLEVLGSKFEGGS-----LPSNESCIRGFDAGFVIGHS 323
QY 337 SNLYAANLQSLYWASEPQFQDWRWRNQANLIDKEQVPLLKIEEPPSTAGRIAEFTDLL 396
Db 324 SSLFVQFL-L-QINTTSLPSFIKDVFNGLFDLDKSNQDASVDNP----- 368
QY 397 TWRLPLAQATHNLRGLHFKHVFQHPHFTWKTATLDGLPNQLTPSEPHLC--LLDV---- 451
Db 369 -----FYK-YNEH-----SSPYAAQKLLDVVDG 390
QY 452 ---GYLINTSCLPLLOPTRDVLILSLD 476
Db 391 GEDGQ--NVPLHLIOPQRHVDVIFAVD 416

RESULT 11
I54375
gene NF2 protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Aug-1999
C:Accession: I54375
R:Arakawa, H.; Hayashi, N.; Nagase, H.; Ogawa, M.; Nakamura, Y.
Hum. Mol. Genet. 3, 565-568, 1994
A>Title: Alternative splicing of the NF2 gene and its mutation analysis of breast and co
A:Reference number: I54375; MUID:94348501; PMID:8069299
A:Accession: I54375
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Cross-references: GB:S73853; NID:G688372; PIDN:AAB31736.1; PID:G688373
C:Genetics:
A:Gene: GDB:NF2
A:Cross-references: GDB:I20232; OMIM:101000
A:Map position: 22q12.2-22q12.2
C:Superfamily: Integrin beta chain; laminin-type EGF-like homology

Query Match 5.3%; Score 170; DB 2; Length 46;
Best Local Similarity 76.7%; Pred. No. 1.2e-06;
Matches 33; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 41 FMEESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
Db 4 FNCESSVTLAGVQWRDLGLQLPLPKFKRFSCLSPSSWDYR 46

RESULT 12
S53037
PLB1 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YMR270.10c; protein YMR008c
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999
C:Accession: S53037; A53647
R:Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53028
A:Accession: S53037
A:Molecule type: DNA
A:Residues: 1-664 <DEV>
A:Cross-references: EMBL:Z48613; NID:G728645; PIDN:CAA88523.1; PID:G728655; MIPS:YMR008c
A:Experimental source: strain AB972
R:Lee, K.S.; Patton, J.L.; Fido, M.; Hines, L.K.; Kohlwein, S.D.; Palttauf, F.; Henry, S.
J. Biol. Chem. 269, 19725-19730, 1994
A>Title: The Saccharomyces cerevisiae PLB1 gene encodes a protein required for lysophosph
A:Reference number: A53647; MUID:94327513; PMID:8051052
A:Accession: A53647
A:Molecule type: DNA
A:Residues: 1-31, 'S', 33-493, 'D', 495-664 <LEE>
A:Cross-references: GB:I23089; NID:G437731; PIDN:AAA61611.1; PID:G437732
A>Note: the authors translated the codon GAC for residue 494 as Glu
```

```
C:Genetics:
A:Gene: SGD:PLB1
A:Cross-references: SGD:S0004610; MIPS:YMR008c
A:Map position: 13L
C:Superfamily: yeast lysophospholipase
C:Keywords: transmembrane protein
F:648-664/Domain: transmembrane #status predicted <TM>

Query Match 5.0%; Score 162; DB 2; Length 664;
Best Local Similarity 21.5%; Pred. No. 0.00022;
Matches 96; Conservative 64; Mismatches 170; Indels 116; Gaps 20;

QY 89 VRLGFGPCAEQAFLSRR-----KQVVAALRALQALQDGL-----QEDEIFVVALM 135
Db 43 VREASGLSDNETEWLKKRDATYKHALHPLNRATSNFSDTSLSTLFGSNSSNMPKIAVA 102
QY 136 ATGGGIRAMTSLYGQLAGLKEL-----GLLDCVSYITCAGSTWALANLYEDPEW 185
Db 103 CSGGGYRAMLSGAGMLAAMDNRDTGANEHGLGLGGLGATYLAGLGGNWLSTLAWN-NW 161
QY 186 SQKDLAGPTELLKTKVTQKNKGLVLAQPSQLQRYR-----QELAERARLGYPSCTNL 236
Db 162 TSVQALVDNTTESNSIWDISHSILTPDGINIFKTGSRWDDISDDVDKDKDAGFNISLADV 221
QY 237 WALINEAL-----LHDEPHDKLSDQREA--LSHGQNPLPI-----YCALNTKGQSL 281
Db 222 W---GRALAYNFWPSLHRGGVGVTWSTLREADVFKNGEMPPFITVADGRYPGTTVINLA 278
QY 282 TTFFEGCEWCEFSYEVGF--PKYGAIPSELFGSEFFMGQMKRLPESRICFLEGWSNL 339
Db 279 TLF-----EFNPFEGMSWDPTLNATDVYLGTVNTGK-----PVNKGQCIAGFDNTG 327
QY 340 YAANLQDSLWASEPQFQDWRWRNQANLIDKEQVPLLKIEEPPSTAGRIAEFTDLLTWR 399
Db 328 FITATSSTLF-----NQF-----LLRLNS-----TDLPSF- 352
QY 400 PLAAQATHNLRGLHFKH-----YFQHPHSTWKTATLDGLPNQLTPSEPHLCILDV 451
Db 353 -IANLATDFLEDLSNDDIAIYAPNPFKEANFLQKNAT-----SSIIIESE-YLFLVDG 404
QY 452 GY-LINTSCLPLLOPTRDVLILSLD 476
Db 405 GEDNQNIPLVPLLLQKEREIDVIFALD 430

RESULT 13
I54374
gene NF2 protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: I54374
R:Pykett, M.J.; Murphy, M.; Harnish, P.R.; George, D.L.
Hum. Mol. Genet. 3, 559-564, 1994
A>Title: The neurofibromatosis 2 (NF2) tumor suppressor gene encodes multiple alternativ
A:Reference number: I54374; MUID:94348500; PMID:8069298
A:Accession: I54374
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-39 <RES>
A:Cross-references: GB:L27065; NID:G463120; PIDN:AAA62422.1; PID:G463121
C:Genetics:
A:Gene: GDB:NF2
A:Cross-references: GDB:I20232; OMIM:101000
A:Map position: 22q12.2-22q12.2
C:Superfamily: Integrin beta chain; laminin-type EGF-like homology

Query Match 4.9%; Score 160; DB 2; Length 39;
Best Local Similarity 79.5%; Pred. No. 5.4e-06;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 45 SLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
Db 1 SCSVTLAGVQWRDLGLQLPLPKFKRFSCLSPSSWDYR 39
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 19:13:29 ; Search time 24.2 Seconds
(without alignments)
1301.754 Million cell updates/sec

Title: US-09-830-321A-2

Perfect score: 3235

Sequence: 1 MIFVLSPTIALCLERVASH.....EQLEALROAVRRQRPH 605

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	619	19.1	749	PA24_HUMAN	P47712 homo sapien
2	611.5	18.9	749	PA24_HORSE	O77793 equus caball
3	599.5	18.5	748	PA24_MOUSE	P47713 mus musculus
4	596	18.4	748	PA24_CHICK	P49147 gallus gall
5	594	18.4	752	PA24_RAT	P50393 rattus norv
6	572	17.7	741	PA24_BRARE	P50392 brachydanio
7	226.5	7.0	591	ALU8_HUMAN	P39195 homo sapien
8	199.5	6.2	587	ALU2_HUMAN	P39189 homo sapien
9	199.5	6.2	593	ALU7_HUMAN	P39194 homo sapien
10	198	6.1	587	ALU3_HUMAN	P39190 homo sapien
11	192.5	6.0	593	ALU6_HUMAN	P39193 homo sapien
12	191	5.9	585	ALU5_HUMAN	P39192 homo sapien
13	186	5.7	673	PLB4_SCHPO	O99327 schizosacch
14	184	5.7	686	PLB3_YEAST	O08108 saccharomyc
15	182	5.6	591	ALU1_HUMAN	P39188 homo sapien
16	177.5	5.5	649	PLB1_TORDE	Q11121 torulaspora
17	177	5.5	612	PLB1_PENCH	P39457 penicillium
18	172.5	5.3	659	PLB1_CANGA	O8tg07 candida gla
19	165.5	5.1	608	PLB2_CANAL	O93795 candida alb
20	164	5.1	605	PLB1_CANAL	Q9uwi6 candida alb
21	164	5.1	626	PLB_NEUCR	O42790 neurospora
22	162	5.0	640	PUB_KULLA	O59863 kluyveromyc
23	162	5.0	664	PLB1_YEAST	P39105 saccharomyc
24	159.5	4.9	633	PLB5_SCHPO	O9y7n6 schizosacch
25	159	4.9	624	PLB2_SCHPO	O19857 schizosacch
26	154	4.8	754	PLB3_CANAL	Q9uwx1 candida alb
27	151	4.7	613	PLB1_SCHPO	P78854 schizosacch
28	146.5	4.5	695	PLB2_CANGA	O8tg06 candida gla
29	143.5	4.4	603	ALU4_HUMAN	P39191 homo sapien
30	140	4.3	644	PLB6_SCHPO	Q9uth5 schizosacch
31	136	4.2	706	PLB2_YEAST	Q03674 saccharomyc
32	122	3.8	536	SP01_YEAST	P35541 saccharomyc
33	105	3.2	431	VGF_BPPHK	Q38041 bacteriophag

34	103	3-2	432	1	NPX2_RAT	P97738 rattus norv
35	101.5	3-1	946	1	RHG4_HUMAN	P98171 homo sapien
36	100.5	3-1	1138	1	RDL3_ARATH	Q8w3k0 arabidopsis
37	99.5	3-1	664	1	Y4FB_RHISN	P55440 rhizobium s
38	99.5	3-1	1026	1	EX5B_CHLMU	Q9plt8 chlamydia m
39	99	3-1	690	1	VATI_DEIRA	Q9rwh3 deinococcus
40	99	3-1	4473	1	PLE1_CRIGR	Q9ji55 cricetus
41	99	3-1	4687	1	PLE1_RAT	P30427 rattus norv
42	98.5	3-0	2208	1	POLN_MANCV	Q69014 manchester
43	98	3-0	438	1	SGCE_HUMAN	O43556 homo sapien
44	97	3-0	852	1	POL_BLVAV	P25059 bovine leuk
45	96.5	3-0	772	1	LMBT_HUMAN	Q9y468 homo sapien

ALIGNMENTS

RESULT 1
PA24_HUMAN
ID PA24_HUMAN STANDARD; PRT; 749 AA.
AC P47712;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytosolic phospholipase A2 (CPLA2) [Includes: Phospholipase A2
[EC 3.1.1.4] (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
[EC 3.1.1.5]].
DE PLA2G4A OR PLA2G4 OR CPLA2.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91256305; PubMed=1904318;
RA Clark J.D., Lin L.-L., Kriz R.W., Ramesha C.S., Sultzman L.A.,
RA Lin A.Y., Milona N., Knopf J.L.;
RT "A novel arachidonic acid-selective cytosolic PLA2 contains a Ca(2+)-
dependent translocation domain with homology to PKC and GAP.";
RL Cell 65:1043-1051(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311987; PubMed=1869522;
RA Sharp J., White D., Chiou G., Goodson T., Gamboa G., McClure D.,
RA Burgett S., Hoskins J., Skatrud P., Sportsman J., Becker G., Kang L.,
RA Roberts E., Kramer R.;
RT "Molecular cloning and expression of human Ca(2+)-sensitive cytosolic
phospholipase A2.";
RL J. Biol. Chem. 266:14850-14853(1991).
RN [3]
RP SEQUENCE OF 1-186 FROM N.A.
RA Howden P.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP MUTAGENESIS OF SER-505, AND PHOSPHORYLATION BY MAP KINASE.
RX MEDLINE=93145328; PubMed=8381049;
RA Lin L.-J., Wartman M., Lin A.Y., Knopf J.L., Seth A., Davis R.J.;
RT "cPLA2 is phosphorylated and activated by MAP kinase.";
RL Cell 72:269-278(1993).
RN [5]
RP MUTAGENESIS OF SER-228.
RX MEDLINE=94299545; PubMed=8027085;
RA Sharp J.D.;
RL Unpublished results, cited by:
RL Nalefski E.A., Sultzman L.A., Martin D.M., Kriz R.W., Towler P.S.,
RL Knopf J.L., Clark J.D.;
RL J. Biol. Chem. 269:18239-18249(1994).
RN [6]
RP INTERACTION WITH HTATIP.
RX MEDLINE=21309279; PubMed=11416127;
RA Sheridan A.M., Force T., Yoon H.J., O'Leary E., Choukroun G.,
RA Taheri M.R., Bonventre J.V.;
RT "PLIP, a novel splice variant of Tip60, interacts with group IV

cytosolic phospholipase A(2), induces apoptosis, and potentiates prostaglandin production.";
 RL Mol. Cell. Biol. 21:4470-4481 (2001).
 [7]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 16-141.
 RP MEDLINE=98104145; PubMed=9430701;
 RX Perisic O., Fong S., Lynch D.E., Bycroft M., Williams R.L.;
 RA "Crystal structure of a calcium-phospholipid binding domain from
 RT cytosolic phospholipase A2";
 RL J. Biol. Chem. 273:1596-1604 (1998).
 [8]
 RN STRUCTURE BY NMR OF 1-138.
 RP MEDLINE=98332749; PubMed=9665851;
 RX Xu G.-Y., McDonagh T., Yu H.-A., Nalefski E.A., Clark J.D.,
 RA Cumming D.A.;
 RT "Solution structure and membrane interactions of the C2 domain of
 cytosolic phospholipase A2";
 RL J. Mol. Biol. 280:485-500 (1998).
 CC -!- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the
 CC sn-2 position releasing arachidonic acid. Together with its
 CC lysophospholipid activity, it is implicated in the initiation of
 CC the inflammatory response.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
 CC glycerophosphocholine + a fatty acid anion.
 CC -!- ENZYME REGULATION: Stimulated by agonists such as ATP, EGF,
 CC thrombin and bradykinin as well as by cytosolic Ca (2+).
 CC -!- SUBUNIT: Interacts with HTATIP.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane
 CC vesicles in a calcium-dependent fashion.
 CC -!- TISSUE SPECIFICITY: Expressed in various tissues such as
 CC macrophages, platelets, neutrophils, fibroblasts and lung
 CC endothelium.
 CC -!- DOMAIN: The N-terminal C2 domain, by its association with lipid
 CC membranes, mediates the regulation of CPLA2 by presenting the
 CC active site to its substrate in response to elevations of
 CC cytosolic Ca(2+).
 CC -!- PTM: Activated by phosphorylation on a serine residue.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M72393; AAB00789.1; -;
 CC EMBL; M68874; AAA60105.1; -;
 CC EMBL; ALG022147; CAB42689.1; -;
 CC PIR; A39329; A39329.
 CC PDB; 1RLW; 25-FEB-98.
 CC PDB; 1BCJ; 13-JAN-99.
 CC PDB; 1CJY; 20-APR-00.
 CC Genew; HGNC:9035; PLA2G4A.
 CC MIM; 600522; -;
 CC GO; GO:0005929; C:cytosol; NAS.
 CC GO; GO:0016021; C:integral to membrane; NAS.
 CC GO; GO:0004623; F:phospholipase A2 activity; NAS.
 CC GO; GO:0006590; P:icosanoid metabolism; NAS.
 CC GO; GO:0006563; P:platelet activating factor biosynthesis; NAS.
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR008973; C2_CaLB.
 CC InterPro; IPR002642; FLAC.
 CC Pfam; PF01168; C2; 1.
 CC Pfam; PF01735; PLA2_B; 1.
 CC SMART; SM00239; C2; 1.
 CC SMART; SM00022; FLAC; 1.
 CC PROSITE; PS00004; C2_DOMAIN_2; 1.
 CC Hydrolase; Lipid degradation; Calcium; Phosphorylation; 3D-structure.
 KW
 RN DOMAIN 1 178 PHOSPHOLIPID BINDING (PROBABLE).

FT	DOMAIN	5	106	C2 DOMAIN.
FT	MOD RES	505	505	PHOSPHORYLATION (BY MAPK).
FT	MUTAGEN	228	228	S->A: ABOLISHES BOTH PHOSPHOLIPASE AND
FT				LYSOPHOSPHATASE ACTIVITY.
FT	MUTAGEN	505	505	S->A: DECREASES AGONIST-STIMULATED
FT				RELEASE OF ARACHIDONIC ACID.
FT	SEQUENCE	749	85210	MW; 9F9CDC5A98231C70 CRC64;
QY	Query Match		19.1%;	Score 619; DB 1; Length 749;
QY	Best Local Similarity		27.1%;	Pred. No. 4.4e-40;
Db	Matches 174; Conservative		125; Mismatches 238; Indels 106; Gaps 22;	
QY		44	ESLSVAQAGVQWRDLGSLQPPPLGPKFSCLSLSSWDYRLRELA----	VLRFQPCAAE 99
Db		100	ETLGTATFTVSSMKVGEKVEFFIFNQVTEVLEMS-----	LEVCSCLPRLPSMALCQDE 154
QY		100	QAFLSRRKQVVAALRQAL---QLDGLQDEIPVVAIMATGGGIRAMTSYGLQLAGLKE	156
Db		155	KTFQQRKEHRESMKULGPNSEGLHSARDVPVAILGSGGFRAMVGFSGVMKALYE	214
QY		157	LGLLDCVSIITGASGWTWALNLYDEPWSQKDLAGPTL---	LKTQVTKNKLGVAPSQ 213
Db		215	SGILDCATYVAGLSGWTWSTLYSHDPPEK--	GPEINEELMKVSHNPLLLTPQK 271
QY		214	LQRYQELAEARALGYPSCFTNLWA--LINEALLHDEPHDKLSQREALSHGONPLIYC	272
Db		272	VKRYVESLWKKKSGQPVTFDFGLMIGETLIHNRMT--	TLSSLUKVKVNTAQCPPLPFT 330
QY		273	ALNTKQSLITTFEGCEWCEFSYEVGPKYGAIPSELFSGSEFFMGQMLKRLPESRICPL	332
Db		331	CUHVK--PDVSELMFADWVEFSYEIGMAKYGTFMADPLFGSKFFMGTVVKYEEPLHFL	389
QY		333	EGIMSNLYA-----ANLQDSLYWASEPFSQFWDWRVWRNOANLDKQVPLL	376
Db		390	MGVGSASFILNRLVGLVSGSQSRGSTMEEEL-----	ENITTKHIVSNDSDSD-- 439
QY		377	KTEBPPSTAGRIA--EFTD-----	LLTWRLPAQATHNFLRLGPHF 415
Db		440	ESHEPKGTENEDAGSDYQSDNQASWIHRMIMALVSDSALFNTREGRAKGKVMFLGLNLN	499
QY		416	KDYFQHP--HFSTWKATLLDGL-----	PNQ-----LTPSEPHCLLDVGYLINTSCL 460
Db		500	TSYPLSPSLSDFAQDSFDDDELDAVADDEFEIYEPDLVSKKHVVDSGLTFNLVYP	559
QY		461	PLIQPTRDVLILSLDYNLHGA-----	FQOLQLGRFCQEQIPPPPIPSPEEQLOPRE 515
Db		560	LILRQRGVDLIIISDFPSARPSDSSPPFKELLAEKWKMKLPPFKIDYVDFDREGLKE	619
QY		516	CHTFSDPTCP---GAPAVLHF-----	SSGV--RTPEEAAAGEVNL--SSSDSPY 558
Db		620	CYVFK--PKNPDMEKDCFTTIHFVLANINFRKYKAPGVPRETBEKEIAFDIDDPESPFP	678
QY		559	HYTKVTSOEDVDKLLHLTHYVNCNNOELLEALRAQVQRRRQ	601
Db		679	STFNFOYPNQAFKRLHDLMEFNTLNNIDIVKEAMVESIEVRRQ	721
RESULT 2				
PA24_HORSE				
ID	PA24_HORSE	STANDARD;	PRT;	749 AA.
AC	O77793;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Cytosolic phospholipase A2 (CPLA2) [Includes: Phospholipase A2			
DE	(EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase			
DE	(EC 3.1.1.5)]			
GN	PLA2G4A OR PLA2G4 OR CPLA2.			
OS	Equus caballus (Horse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
OX	NCBI_TaxID=9796;			
RN	[1]			

SEQUENCE FROM N.A.
 TISSUE=Neutrophils;
 RA Larsson Forsell P.K.A., Lindberg A., Karlsson S., Lindgren J.A.,
 RA Claesson H.-E.;
 RT "Purification, characterization and cDNA sequencing of calcium-
 dependent cytosolic phospholipase A2 from equine neutrophils.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC !- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the
 CC sn-2 position releasing arachidonic acid. Together with its
 CC lysophospholipid activity, it is implicated in the initiation of
 CC the inflammatory response.
 CC !- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC !- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
 CC glycerophosphocholine + a fatty acid anion.
 CC !- ENZYME REGULATION: Stimulated by agonists such as ATP, EGF,
 CC thrombin and bradykinin as well as by cytosolic Ca(2+) (By
 CC similarity).
 CC !- SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane
 CC vesicles in a calcium-dependent fashion (By similarity).
 CC !- DOMAIN: The N-terminal C2 domain, by its association with lipid
 CC membranes, mediates the regulation of CPLA2 by presenting the
 CC active site to its substrate in response to elevations of
 CC Cytosolic Ca(2+) (By similarity).
 CC !- PTM: Activated by phosphorylation on a serine residue (By
 CC similarity).
 CC !- SIMILARITY: Contains 1 C2 domain.
 CC
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 CC
 CC EMBL; AF092539; AAC61774.1; -;
 CC HSSP; P47712; 1BCI.
 CC InterPro; IPR000008; C2.
 CC InterPro; IPR008973; C2_CaLB.
 CC InterPro; IPR002642; PLAC.
 CC Pfam; PF00168; C2; 1.
 CC Pfam; PF01735; PLA2_B; 1.
 CC SMART; SM00239; C2; 1.
 CC SMART; SM00022; PLAC; 1.
 CC PROSITE; PS00004; C2_DOMAIN_2; 1.
 CC Hydrolase; Lipid degradation; Calcium; Phosphorylation.
 KW DOMAIN 1 178 PHOSPHOLIPID BINDING (PROBABLE).
 FT DOMAIN 1 178
 FT MOD_RES 505 505 C2 DOMAIN.
 FT MOD_RES 505 505 PHOSPHORYLATION (BY MAPK) (BY
 FT SIMILARITY).
 FT SEQUENCE 749 AA; 85454 MW; 493A67DF28D50FE0 CRC64;
 Query Match 18.9%; Score 611.5; DB 1; Length 749;
 Best Local Similarity 27.8%; Pred. No. 1.7e-39;
 Matches 165; Conservative 121; Mismatches 212; Indels 95; Gaps 21;
 QY 89 VRLGFGCAEEQAFLSRRKQVVAALRQAL---QLDGLQDEIPVVAIMATGGGIRAWT 145
 DB 144 LRFSMALCDQETFRQQRKENIKENKILLGPKKSEGLYSTRDVPVAILGSGGGFRAMV 203
 QY 146 SLYGLAGLKEGLDLCVSYITGASGSTWALANLYEDPEWSQKDLAGPEL---LKTQVT 202
 DB 204 GFSGVWKALYESGILDCAITLGLSSGSSWYMTLSHDPFPPK---GPEINKELMKVVS 260
 QY 203 KKNLGVLPASQIQRYQELAEARLIGYSCFTNLWA-LINEALLHDEPHDKLSQREAL 261
 DB 261 YDPLLLLTQPKIKRYVESLWKKSSQPVTFDIFGLMIGETLIHNRMT-TLSLKEKV 319
 QY 262 SHQNPLPYCALNTKGQSLITTFECGCEPSYVGGPKYCAFIPTSELFGSEFFMGQIM 321
 DB 320 NTAQCPPLTLFTLHVK-PDVSELMFADWVFSPYBIGMAKYGTFMAPDLFGSKFFMGTV 378

QY 322 KRLPESRICFLEGINLWNLAAANLQDSLYWASEPSQFQWRVNRQANLDKEQVLL----- 376
 DB 379 KKYEENPLHLFMGVGSAFSILFRNLVGVSGS-----QNGSTMEELNITAKHI 429
 QY 377 -----KIEEPPSTAGRIAE--FFTD-LLTW-RPL-----AAQT 405
 DB 430 VNSDSSDSDDESEPKGTENEDAEADRYQNDNQASVHMLMALVSDSALENTREGRAKV 489
 QY 406 HNFLRGLHFKHFOYQHP--HFSTWKAATLDGL-----LTPSEPHICLLD 450
 DB 490 HNFMLGLNLNTSYPLSLFRNFTQESLDDDDDLDAVADPDEFERIEPLDVKSKIHVD 549
 QY 451 VGVLTNTSCLPLQOPTRDVLILSLDYNLHGA-----FOQLQLGRFCQEQGPPFPISP 505
 DB 550 SGUTFMPLPYPLILRPGQGVDLIISFDSARPSDSSPPFKELLALAEKWKAKMLKLPFKIDP 609
 QY 506 SPEEQQPRECHTFSDPTCP---GAPAVLHF-----SSGV-RTTPEAAAGEV 549
 DB 610 YVFDREGLKECVFK-PKNPDVEKDCPTIIHFVLANINFRKYKAPGVPRETKEELADF 668
 QY 550 NL-SSDSYHYTKVYSQEDVDKLLHLTHYVNNQEQQLLEALQAVQRRRQ 601
 DB 669 DIFDDPESPSTFNFQYPNQAFKRLHDLMEFNTLNNIDVIKNAWVESIEYRRQ 721
 RESULT 3
 PA24_MOUSE
 ID PA24_MOUSE STANDARD; PRT; 748 AA.
 AC P47713;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cytosolic phospholipase A2 (CPLA2) [Includes: Phospholipase A2
 DE (EC 3.1.1.4) [Phosphatidylcholine 2-acylhydrolase]; Lysophospholipase
 DE (EC 3.1.1.5)].
 GN PLA2G4A OR PLA2G4 OR CPLA2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91256305; PubMed=1904318;
 RA Clark J.D., Lin L.-L., Kriz R.W., Ramesha C.S., Sultzman L.A.,
 RA Lin A.Y., Milona N., Knopf J.L.;
 RT "A novel arachidonic acid-selective cytosolic PLA2 contains a Ca(2+)-
 RT dependent translocation domain with homology to PKC and GAP.";
 RL Cell 65:1043-1051(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC !- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the


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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U10329; AAA53228.1; -.
CC PIR; I50699; I50699.
CC HSSP; P47712; 1BCI.
CC InterPro; IPR000008; C2.
CC InterPro; IPR008973; C2_CaLB.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF01735; PLA2_B; 1.
CC SMART; SM00239; C2_1.
CC SMART; SM00222; PLA2; 1.
CC PROSITE; PS00004; C2_DOMAIN_2; 1.
KW Hydrolyase; Lipid degradation; Calcium; Phosphorylation.
FT DOMAIN 1 178 PHOSPHOLIPID BINDING.
FT DOMAIN 5 106 C2 DOMAIN.
FT MOD_RES 505 505 PHOSPHORYLATION (BY MAPK) (BY
FT SIMILARITY).
SQ SEQUENCE 748 AA; 84978 MW; 996A5256CA032F75 CRC64;
Query Match 18.4%; Score 596; DB 1; Length 748;
Best Local Similarity 25.9%; Pred. No. 2.7e-38;
Matches 166; Conservative 129; Mismatches 245; Indels 100; Gaps 20;
QY 44 ESLSVAQAQGVQWEDIGSLQPPGLGKRFSCLSLPSWDYRLRELAVRLGFGPCAERQAF 103
DB 100 ETLGWATFPISLKLGEKEVQLTFNNVTMTLESLV-CSSTDRLFSMALCDEKKFR 158
QY 104 SRKQVVAALQAQLQDGD---LQDEIPVVAIMATGGIRAMTSLYQLAGLKELGLL 160
DB 159 QQRKNIMOSMKFFGEENSKNLTTSRDVPIAVLGGSGGFRAMVGFAGVMKALYESGVL 218
QY 161 DCVSYITGASGTWALANLYEDPEWSQKOLLAGPTL---LKTQVTKNLGLVLAPOLOQRY 217
DB 219 DCATYIAGLSGTWYMTSLYSHDPFEK---GPKNEQLMSVSNPLLLTPQVKRY 275
QY 218 RELAEARLGVPSCTNLA-LINALLHDPHDKLSDOREALSHGQNPFIYCALNT 276
DB 276 IEALWNKSGSGOPVTFTDFGLIGETLIHNR-MDTTSLDMKEKVEAQCALPLFTCLHV 334
QY 277 KQSLTTFEGWCESPVEVGFPPKYGATIPELFGSEFFMQLMKRLPESRICFLEGW 336
DB 335 K-PDVSLELFAOWVEFSPEIGWAKYGTGTFMSPDLFGSKFFMGTVVKKYGENPLHFLMGVY 393
QY 337 SNLYAANLDQSLYWAESPQFWDWRVNRQANLDKEQVPLLKI-----EPP 381
DB 394 GSASFILNRLVGVNS-----QNGPTWEELENIKHLVNSDSSDESQHP 444
QY 382 PSTAGRIA-----EFFTDL-----TWRLAQATHNRLRGLHFKDYFQ 420
DB 445 KGTENSEANEYQNSQESWQVQMLMALVGDALFNTRGRAGKVHNFMLGLNLNSCYPL 504
QY 421 HP--HFSTWKATTLQGL-----PQ-----LTPSEPHLCLLDVGYLINTSCLP 465
DB 505 SPLADLLTQESVEEDELDAADDPDEFRIYPLDVSKXKHIVDSGLTFNLPYPLILRP 564
QY 466 TRVDLLILSLDNLHGA-----FOQLQLLGRFCQEGIPFPPIPSPERQLQPRECHTF- 519
DB 565 QRGVDLIISDFRSARPSDSSPPFKELLAEKAKKNKLFPFKIDNVFREGKCYVPK 624
QY 520 -----SDTPCQAPAVLHF-----SSGV-RRTEPEAAAGEVNI-SSSDSPYHYT 561
DB 625 PKDTSEKDC---PTIHFVLANINFRKYKAPGLPRESKEKDFADFDIDDPNTPFSFF 681
QY 562 KVTYSQEDVDKLLHLYHNVQCNQQLLEALQAQVRRQ 601
DB 682 NFQYPNEAFKRLHDLMEFNTLNLNDLVIKQAMMESIEYRKE 721
RESULT 5
PA24_RAT
ID PA24_RAT
AC P50393;

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DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytosolic phospholipase A2 (CPLA2) [includes: Phospholipase A2
DE (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
DE (EC 3.1.1.5)].
GN PLA2G4A OR PLA2G4 OR CPLA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Brain;
RA Owada Y., Tomimaga T., Yoshimoto T., Kondo H.;
RT "Molecular cloning of rat cDNA for cytosolic phospholipase A2 and the
RT increased gene expression in the dentate gyrus following transient
RT forebrain ischemia.";
RL Brain Res. Mol. Brain Res. 25:364-368(1994).
RN [2]
RP ERRATUM.
RX MEDLINE=95206125; PubMed=7898324;
RA Owada Y., Tomimaga T., Yoshimoto T., Kondo H.;
RL Brain Res. Mol. Brain Res. 27:355-355(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pancratic islets;
RX MEDLINE=98223459; PubMed=9555100;
RA Ma Z., Ramanadham S., Hu Z., Turk J.;
RT "Cloning and expression of a group IV cytosolic Ca2+-dependent
RT phospholipase A2 from rat pancreatic islets. Comparison of the
RT expressed activity with that of an islet group VI cytosolic Ca2+-
RT independent phospholipase A2.";
RL Biochim. Biophys. Acta 1391:384-400(1998).
CC -!- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the
CC sn-2 position releasing arachidonic acid. Together with its
CC lysophospholipid activity, it is implicated in the initiation of
CC the inflammatory response.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC glycerophosphocholine + a fatty acid anion.
CC -!- ENZYME REGULATION: Stimulated by agonists such as ATP, EGF,
CC thrombin and bradykinin as well as by cytosolic Ca(2+).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane
CC vesicles in a calcium-dependent fashion (By similarity).
CC -!- TISSUE SPECIFICITY: In brain tissue, expressed in low levels in
CC olfactory mitral and granule cells, in hippocampal pyramidal
CC cells and in dentate and cerebellar granule cells.
CC -!- INDUCTION: Levels of rat CPLA2 are increased in dentate granule
CC cells during ischemia.
CC -!- DOMAIN: The N-terminal C2 domain, by its association with lipid
CC membranes, mediates the regulation of CPLA2 by presenting the
CC active site to its substrate in response to elevations of
CC cytosolic Ca(2+) (By similarity).
CC -!- PTM: Activated by phosphorylation on a serine residue (By
CC similarity).
CC -!- SIMILARITY: Contains 1 C2 domain.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S77829; AAB33847.1; -.
CC EMBL; U38376; AAC21591.1; -.
CC HSSP; P47712; 1BCI.
CC InterPro; IPR000008; C2.
CC InterPro; IPR008973; C2_CaLB.
CC InterPro; IPR002642; PLA2.

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Db 138 LRFSTMLCDQKLFMTQTRDRVMSIKKLLKMNPRFLPSPREVPITAILGGGFRAM 197
QY 145 TSLYGOLAGLKEGLGLDCVSYITGASSTWALANLYEDPEWSOKDLAGPTL---LKTQV 201
Db 198 VGFSGVWKALYEGVDFCAIYVAGLSGSTWYMSLMYSHPEPAK---GPGDINKELMNRV 254
QY 202 TRNKLGLVAPSOQLORYQELAEARLGYPCFTNLWA-LINEALLHDEPHDKLSQOREA 260
Db 255 SNNPLKLLPQINRYVKALWKKSAGQPTVTFDIFQMLIGETLIFGR-WNKKLSLKGK 313
QY 261 LSHQNPPIYCALNTKGSLTTFEFGWCFSPYVGPFGYAGTIPSELFGSEFFMQGL 320
Db 314 INEGOSPLFLFTCLHVK-PDVSLMFADWVEFSPYBGMKAYGTFSPLFGSKFFMGSV 372
QY 321 MKRLPSRCLFGLGWSNLY-----AANLQDSLYWASEPSQFWDVRVRNQ 365
Db 373 VQKYENPHLPLMGWGSFAFSLFNVLGVKETTSSSTMEEELEQIKPEHIVGDDSDNE 432
QY 366 ANLDK---EQVPLLKIEPPSTAGRIAEFFTDLL-----TWRLAQATHNLRGLHFH 415
Db 433 EETQRGTSADAEDERQORHAQSWQVRLTSMGTTLFTTREGRAKGVNPNMGLNLN 492
QY 416 KYDFQHPHSTKATILDLGNLQLT-PSE-----PHLCULLDVGYLINTSCPLP 462
Db 493 STLPPSPFGSITHOTSLEEVDAVTDPEFERIYEPDLVKSKKHVVDVSGLTFLNLPYLI 552
QY 463 LQPTRVDVILSLDYNLHGA-----FQQLQLLGRFCQEGIPPPISPSPEQLQPRECH 517
Db 553 LRCQGVLDLIIIFDSARSFSSPPPKELLAEKWMKMLPPPKIDSKVDFREGUKEY 612
QY 518 TF-----SDPTCPGAPAVLHF-----SSGV-RRTPPEAAAGEVNL-SSSDSPYHY 560
Db 613 VFPAKGDKNK---PTLIHVLANINFRNFKAPGVPRDSKDIEFGDFDIFDEPASPYST 669
QY 561 TKVTSQEDVDKLLHLTHVNCNQBOLLEALRQAVQRRQ 601
Db 670 FNFYNNQAFKRLHDLMEFTNLNIEVIKEAKDSILLRRE 710

RESULT 7
ALU8 HUMAN
ID ALU8 HUMAN STANDARD; PRT; 591 AA.
AC P39195;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alu subfamily SX sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=95021758; PubMed=7935834;
RA Claverie J.-M.; Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN (2)
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
RT potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN (3)
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation
RT closely connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN (4)

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RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
CC THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC REPEATS.
CC -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC CODON, 'XX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further
CC pollution of protein sequence databases with Alu-derived amino
CC acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC primate genomes with an average spacing of 4 kb. Some of them are
CC actively transcribed by pol III. Normal transcripts may contain
CC Alu-derived sequences in 5' or 3' untranslated regions. However,
CC CDNA libraries also contain partial and/or rearranged cDNAs
CC ligated with Alu-derived sequence in any orientation. Although Alu
CC elements (especially situated on the complementary strand) have a
CC great potential to create additional/alternative exons,
CC consideration should be given to the possibility that the presence
CC of an Alu in an open reading frame may have resulted from a
CC cloning artifact or may be due to misinterpretation of sequencing
CC data. This point has been overlooked on several occasions, with
CC the consequence of erroneous Alu-derived amino acid sequences
CC being reported.
CC -!- CAUTION: Any significant similarity of a putative protein sequence
CC with an Alu-translated entry must be taken as a warning that a
CC part of Alu repeat may have been artifactually included in the
CC coding nucleotide sequence.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U14574; -; NOT_ANNOTATED_CD.
CC DR Hypothetical protein.
CC FT DOMAIN 1 96 FRAME-1.
CC FT DOMAIN 100 195 FRAME-2.
CC FT DOMAIN 100 195 FRAME-3.
CC FT DOMAIN 298 393 FRAME-4.
CC FT DOMAIN 397 492 FRAME-5.
CC FT DOMAIN 496 591 FRAME-6.
CC SQ SEQUENCE 591 AA; 64395 MW; AC8154AD8A6BB280 CRC64;

Query Match 7.0%; Score 226.5; DB 1; Length 591;
Best Local Similarity 65.3%; Pred. No. 8.8e-10;
Matches 47; Conservative 1; Mismatches 17; Indels 7; Gaps 1;

QY 32 PAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE----- 86
Db 488 PASARXXXFFETESRSVAQAGVQWRDLGSLQPPPPGFKRFSCLSLPSSWDYRAPPRPAN 547
QY 87 --LAVRLGFGPC 96
Db 548 FCIFSRDGVSPC 559

RESULT 8
ALU2 HUMAN
ID ALU2 HUMAN STANDARD; PRT; 587 AA.
AC P39189;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alu subfamily SB sequence contamination warning entry.

```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95021758; PubMed=7935834;
 RX Claverie J.-M., Makalowski W.;
 RA "Alu alert.";
 RL Nature 371:752-752(1994).
 RN [2]
 RN CONCEPT.
 RP MEDLINE=92241891; PubMed=1572661;
 RX Claverie J.-M.;
 RA "Identifying coding exons by similarity search: alu-derived and other
 RT potentially misleading protein sequences.";
 RL Genomics 12:838-841(1992).
 RN [3]
 RP ALU FAMILIES CLASSIFICATION.
 RP MEDLINE=88333009; PubMed=3138422;
 RX Quantin Y.;
 RA "The Alu family developed through successive waves of fixation
 RT closely connected with primate lineage history."
 RL J. Mol. Evol. 27:194-202(1988).
 RN [4]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=91178815; PubMed=1706781;
 RA Jurka J., Milosavljevic A.;
 RT "Reconstruction and analysis of human Alu genes.";
 RL J. Mol. Evol. 32:105-121(1991).
 CC -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
 CC THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
 CC CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
 CC FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
 CC REPEATS.
 CC -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
 CC CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
 CC -!- CAUTION: This Alu entry is provided in order to avoid the further
 CC pollution of protein sequence databases with Alu-derived amino
 CC acid sequences.
 CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
 CC primate genomes with an average spacing of 4 kb. Some of them are
 CC actively transcribed by pol III. Normal transcripts may contain
 CC Alu-derived sequences in 5' or 3' untranslated regions. However,
 CC cDNA libraries also contain partial and/or rearranged cDNAs
 CC ligated with Alu-derived sequence in any orientation. Although Alu
 CC elements (especially situated on the complementary strand) have a
 CC great potential to create additional/alternative exons,
 CC consideration should be given to the possibility that the presence
 CC of an Alu in an open reading frame may have resulted from a
 CC cloning artifact or may be due to misinterpretation of sequencing
 CC data. This point has been overlooked on several occasions, with
 CC the consequence of erroneous Alu-derived amino acid sequences
 CC being reported.
 CC -!- CAUTION: Any significant similarity of a putative protein sequence
 CC with an Alu-translated entry must be taken as a warning that a
 CC part of Alu repeat may have been artifactually included in the
 CC coding nucleotide sequence.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U14568; -; NOT ANNOTATED_CDS.
 DR
 KW Hypothetical protein.
 FT DOMAIN 1 96 FRAME-1.
 FT DOMAIN 100 194 FRAME-2.
 FT DOMAIN 198 292 FRAME-3.
 FT DOMAIN 296 391 FRAME-4.

FT DOMAIN 395 489 FRAME-5.
 FT DOMAIN 493 587 FRAME-6.
 SQ SEQUENCE 587 AA; 63703 MW; 3EAB3E3E329203 CRC64;
 Query Match 6.2%; Score 199.5; DB 1; Length 587;
 Best Local Similarity 65.6%; Pred. No. 1.1e-07; Indels 7; Gaps 1;
 Matches 42; Conservative 1; Mismatches 14;
 QY 40 FFEMESLSVAQGVQWRDLGSLQPPPLGFKFSCISLPSWDYRLRE-----LAVRLG 92
 Db 493 FFETESRVAQGVQWRDLGSLQAPPPGFTFSCISLPSWDYRPPRPPANFCIFSRDG 552
 QY 93 FGPC 96
 Db 553 VSPC 556
 RESULT 9
 ALU7 HUMAN
 ID ALU7 HUMAN STANDARD; PRT; 593 AA.
 AC P39154;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alu subfamily SQ sequence contamination warning entry.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95021758; PubMed=7935834;
 RA Claverie J.-M., Makalowski W.;
 RT "Alu alert.";
 RL Nature 371:752-752(1994).
 RN [2]
 RN CONCEPT.
 RP MEDLINE=92241891; PubMed=1572661;
 RX Claverie J.-M.;
 RT "Identifying coding exons by similarity search: alu-derived and other
 RT potentially misleading protein sequences.";
 RL Genomics 12:838-841(1992).
 RN [3]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=88333009; PubMed=3138422;
 RA Quantin Y.;
 RT "The Alu family developed through successive waves of fixation
 RT closely connected with primate lineage history."
 RL J. Mol. Evol. 27:194-202(1988).
 RN [4]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE=91178815; PubMed=1706781;
 RA Jurka J., Milosavljevic A.;
 RT "Reconstruction and analysis of human Alu genes.";
 RL J. Mol. Evol. 32:105-121(1991).
 CC -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
 CC THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
 CC CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
 CC FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
 CC REPEATS.
 CC -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
 CC CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
 CC -!- CAUTION: This Alu entry is provided in order to avoid the further
 CC pollution of protein sequence databases with Alu-derived amino
 CC acid sequences.
 CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
 CC primate genomes with an average spacing of 4 kb. Some of them are
 CC actively transcribed by pol III. Normal transcripts may contain
 CC Alu-derived sequences in 5' or 3' untranslated regions. However,
 CC cDNA libraries also contain partial and/or rearranged cDNAs
 CC ligated with Alu-derived sequence in any orientation. Although Alu
 CC elements (especially situated on the complementary strand) have a
 CC great potential to create additional/alternative exons,
 CC consideration should be given to the possibility that the presence
 CC of an Alu in an open reading frame may have resulted from a
 CC cloning artifact or may be due to misinterpretation of sequencing
 CC data. This point has been overlooked on several occasions, with
 CC the consequence of erroneous Alu-derived amino acid sequences
 CC being reported.
 CC -!- CAUTION: Any significant similarity of a putative protein sequence
 CC with an Alu-translated entry must be taken as a warning that a
 CC part of Alu repeat may have been artifactually included in the
 CC coding nucleotide sequence.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U14568; -; NOT ANNOTATED_CDS.
 DR
 KW Hypothetical protein.
 FT DOMAIN 1 96 FRAME-1.
 FT DOMAIN 100 194 FRAME-2.
 FT DOMAIN 198 292 FRAME-3.
 FT DOMAIN 296 391 FRAME-4.

consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with the consequence of erroneous Alu-derived amino acid sequences being reported.

CC -!- CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the coding nucleotide sequence.

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CC EMBL; U14573; -; NOT_ANNOTATED_CDS.

CC KW Hypothetical protein.

CC FT DOMAIN 1 97 FRAME-1.

CC FT DOMAIN 101 196 FRAME-2.

CC FT DOMAIN 200 295 FRAME-3.

CC FT DOMAIN 299 395 FRAME-4.

CC FT DOMAIN 399 494 FRAME-5.

CC FT DOMAIN 498 593 FRAME-6.

CC SEQUENCE 593 AA; 64417 MW; 54A4F50F33A6089F CRC64;

Query Match 6.2%; Score 199.5; DB 1; Length 593;
Best Local Similarity 63.1%; Pred. No. 1.1e-07;
Matches 41; Conservative 1; Mismatches 16; Indels 7; Gaps 1;

QY 39 FFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE-----LAVRL 91
Db 299 FLFRSFLVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRPPRPNFNCIFSRD 358

QY 92 GFGPC 96
Db 359 GVSPC 363

RESULT 10

ALU3 HUMAN

ID ALU3 HUMAN STANDARD; PRT; 587 AA.

AC P3190;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alu subfamily SBI sequence contamination warning entry.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

EN [1]

FP SEQUENCE FROM N.A.

RP MEDLINE=95021758; PubMed=7935834;

RA Claverie J.-M., Makalowski W.;

RT "Alu alert."

RL Nature 371:752-752(1994).

RN [2]

RP CONCEPT.

RX MEDLINE=92241891; PubMed=1572661;

RA Claverie J.-M.;

RT "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences.";

RL Genomics 12:838-841(1992).

RN [3]

RP ALU FAMILIES CLASSIFICATION.

RX MEDLINE=88333009; PubMed=3138422;

RA Quentin Y.;

RT "The Alu family developed through successive waves of fixation closely connected with primate lineage history.";

J. Mol. Evol. 27:194-202(1988).

[4] ALU FAMILIES CLASSIFICATION.

RX MEDLINE=91178815; PubMed=1706781;

RA Jurka J., Milosavljevic A.;

RT "Reconstruction and analysis of human Alu genes.";

RL J. Mol. Evol. 32:105-121(1991)

CC -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU REPEATS.

CC -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.

CC -!- CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino acid sequences.

CC -!- CAUTION: Alu repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' untranslated regions. However, cDNA libraries also contain partial and/or rearranged cDNAs ligated with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons, consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with the consequence of erroneous Alu-derived amino acid sequences being reported.

CC -!- CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the coding nucleotide sequence.

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CC EMBL; U14569; -; NOT_ANNOTATED_CDS.

CC KW Hypothetical protein.

CC FT DOMAIN 1 96 FRAME-1.

CC FT DOMAIN 100 194 FRAME-2.

CC FT DOMAIN 198 292 FRAME-3.

CC FT DOMAIN 296 391 FRAME-4.

CC FT DOMAIN 395 489 FRAME-5.

CC FT DOMAIN 493 587 FRAME-6.

CC SEQUENCE 587 AA; 63573 MW; 85C4155726DEF235 CRC64;

Query Match 6.1%; Score 198; DB 1; Length 587;
Best Local Similarity 86.4%; Pred. No. 1.4e-07;
Matches 38; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 40 FFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
Db 493 FFETESRSVAQAGVQWRDLGSLQAPPFGTFPFCSLPSSWDYR 536

RESULT 11

ALU6 HUMAN

ID ALU6 HUMAN STANDARD; PRT; 593 AA.

AC P39193;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alu subfamily SP sequence contamination warning entry.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Fri Oct 8 10:22:34 2004

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021758; PubMed=7935834;
RA Claverie J.-M., Makalowski W.;
RL "Alu alert."
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation
closely connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
REPEATS.
CC -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further
pollution of protein sequence databases with Alu-derived amino
acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
primate genomes with an average spacing of 4 kb. Some of them are
actively transcribed by pol III. Normal transcripts may contain
Alu-derived sequences in 5' or 3' untranslated regions. However,
cDNA libraries also contain partial and/or rearranged cDNAs
ligated with Alu-derived sequence in any orientation. Although Alu
elements (especially situated on the complementary strand) have a
great potential to create additional/alternative exons,
consideration should be given to the possibility that the presence
of an Alu in an open reading frame may have resulted from a
cloning artifact or may be due to misinterpretation of sequencing
data. This point has been overlooked on several occasions, with
the consequence of erroneous Alu-derived amino acid sequences
being reported.
CC -!- CAUTION: Any significant similarity of a putative protein sequence
with an Alu-translated entry must be taken as a warning that a
part of Alu repeat may have been artifactually included in the
coding nucleotide sequence.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U14572; -; NOT_ANNOTATED_CDS.
DR Hypothetical protein.
KW DOMAIN 1 97 FRAME-1.
FT DOMAIN 101 196 FRAME-2.
FT DOMAIN 200 295 FRAME-3.
FT DOMAIN 299 395 FRAME-4.
FT DOMAIN 399 494 FRAME-5.
FT DOMAIN 498 593 FRAME-6.

SQ SEQUENCE 593 AA; 64603 MW; 136EF344AACD12A2 CRC64;
Query Match 6.0%; Score 192.5; DB 1; Length 593;
Best Local Similarity 61.5%; Pred. No. 3.8e-07;
Matches 40; Conservative 1; Mismatches 17; Indels 7; Gaps 1;
QY 39 FFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE-----LAVRL 91
DB 299 FFLRRSFALVAQAGVQWRDLGSPQPPPPGFKRFSCLSLPSSWDYRHAPPRANFCIFSRD 358
QY 92 GFGPC 96
DB 359 GVSPC 363
RESULT 12
ALU5 HUMAN
ID ALU5 HUMAN STANDARD; PRT; 585 AA.
AC P39192;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alu subfamily SC sequence contamination warning entry.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021758; PubMed=7935834;
RA Claverie J.-M., Makalowski W.;
RT "Alu alert."
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation
closely connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
REPEATS.
CC -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further
pollution of protein sequence databases with Alu-derived amino
acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
primate genomes with an average spacing of 4 kb. Some of them are
actively transcribed by pol III. Normal transcripts may contain
Alu-derived sequences in 5' or 3' untranslated regions. However,
cDNA libraries also contain partial and/or rearranged cDNAs
ligated with Alu-derived sequence in any orientation. Although Alu
elements (especially situated on the complementary strand) have a
great potential to create additional/alternative exons,
consideration should be given to the possibility that the presence
of an Alu in an open reading frame may have resulted from a

```

CC Cloning artifact or may be due to misinterpretation of sequencing
CC data. This point has been overlooked on several occasions, with
CC the consequence of erroneous Alu-derived amino acid sequences
CC being reported.
CC
CC -!- CAUTION: Any significant similarity of a putative protein sequence
CC with an Alu-translated entry must be taken as a warning that a
CC part of Alu repeat may have been artifactually included in the
CC coding nucleotide sequence.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U14571; -; NOT ANNOTATED_CDS.
CC
CC KW Hypothetical protein.
CC FT DOMAIN 1 95 FRAME-1.
CC FT DOMAIN 99 193 FRAME-2.
CC FT DOMAIN 197 291 FRAME-3.
CC FT DOMAIN 295 389 FRAME-4.
CC FT DOMAIN 393 487 FRAME-5.
CC FT DOMAIN 491 585 FRAME-6.
CC SQ SEQUENCE 585 AA; 63957 MW; 46EE8C4F493650A7 CRC64;
CC
CC Query Match 5.9%; Score 191; DB 1; Length 585;
CC Best Local Similarity 31.7%; Pred. No. 4.9e-07;
CC Matches 71; Conservative 20; Mismatches 63; Indels 70; Gaps 10;
CC
CC QY 39 FPFEMESLSVAQGVQWRDGLSGLOPPPLGPKRPSCLSLPSSWDYRLRE-----LAVRL 91
CC Db 393 FFDGVSLL-CRQAGVQWRDGLSGLOPPPLGPKRPSCLSLPSSWDYRRAPPANFCIFSRD 451
CC
CC QY 92 GFGFCABEQAFLSRRKQVAAALRQALQLDGDLDQDEIPVVAIMATGGGIRAMTSLYGQL 151
CC Db 452 GVSPCWP-----GWSRSLDLVIRPPPKVL-----GLQXATAPGXX 489
CC
CC QY 152 AGL-----KEGLDLCVSYITGAGSGTWALANL-----YEDPEWSOKLAGPTE----- 195
CC Db 490 XFETESRSVARLEC-----SCAISAHCNLRPLGSSDSPASASRVAGTGTGARHHAQLI 542
CC
CC QY 196 ---LLKT---QVTKNKLGVLPASQLQRYRQELAEARLGPSCF 233
CC Db 543 FVFLVETGFHHVQDGLDLT-----SXSARLGLPKCW 575
CC
CC RESULT 13
CC PLB4_SCHPO
CC ID PLB4 SCHPO STANDARD; PRT; 673 AA.
CC AC Q9P327;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Putative lysophospholipase C977.09c precursor (EC 3.1.1.5)
CC DE (Phospholipase B).
CC GN SPAC977.09C OR SPAC1348.10C.
CC OS Schizosaccharomyces pombe (Fission yeast).
CC OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC OC Schizosaccharomycetales; Schizosaccharomycetaceae;
CC OC Schizosaccharomycetes.
CC ON NCBI_TaxID=4896;
CC RX [1]
CC RC SEQUENCE FROM N.A.
CC RP STRAIN=972;
CC RX MEDLINE=21848401; PubMed=11859360;
CC RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
CC RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
CC RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
CC RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
CC RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
CC RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jacobs K.,

```

116 QAL-----QLDGLQDEIPVVAIMATGGIPAMTSLYQLAGLKE-----LGLL 160
109 SFISKTGLNVLDKVVNSDGRFAGIAFSGGLRAMVNGGAFNAFSDPSPLSGLL 168
161 DCVSVITGASSTWALANLYEDPEWSQDLAPTELLKTQVTKNKLGLVLAPE-----SQL 214
169 QSAMYISGLSGWLVGSV-----AINNFNIT-YLRDNVWNLHSHVFAFHGDVNIENL 221
215 QRY---ROELAEARLGYPSCTNLWALINLALHDEPHDKLSQDREA----- 260
222 NYNDLRKEIDQKHAGFDCSLTDLW-----GRAL-----SRKLVAERGGPGITYSSMRN 272
261 ---LSHGNPPIPIYCA-----LNTKQSITTFEFGWCCEFSFVEYGFPGYGAFI 306
273 QSWFNADYPPIIIVADSRLEETRAIPANTSIFEFTAYEFTGW-----DNGIK---AFI 323
307 PSELFSGEFFMGQMKRLPESRIC-----FLEGIWSNLYAANLQDSLYWASEPSPFW 358
324 PNEYVGT-----HLLDGVPPDKSCIHNVDNAGFVMTSATLNSFLD-----W 367
359 DRWRNQNANLQDKBQVPLKIEBPPTAGRIABFFDILLTWRLAQATHNRLGLHFKD- 417
368 NENVKKN-----DTYYDIL-----HALLLEDLSKHQDD 394
418 ---YFOHPH---PSTWATTLTDLGNLQNLTPSEPH---LCLLDVGY-LINTSCLPLLOTRD 470
395 IAPENPNQYNTSNTSVNAF-----EPYDIDLVDGGBDRENIPLWPLHQRVD 447
471 LITLSD---YNLHGAFAQLQLGRFCQEQGIPFPISPSPEEQLOPRECHTFSD---PTC 524
448 VFAIDSYN-----DPYGMPLGSSIVATYERVVTFNANKSVDRGFPYI 492
525 GPAPAVLHPSGVRRT-----PEEAAAGEVNLSSDSP-----YHYTKVTYSOE 568
493 PENTIISLGNTRPTFFGCDGKNTTAGNHVDNNTPTLLVYFPNYPWTYISNISTFMS 552
569 DVDKLLHLTHYVNC-----NNOEQLEALROA-VORRRORR 603
553 MODKWANGILENAFMTSTONNESFAVCLALIQSLERK 593

RESULT 14
FLB3_YEAST STANDARD; PRT; 686 AA.
AC Q08108;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lysophospholipase 3 precursor (BC 3.1.1.5) (Phospholipase B 3).
GN FLB3 OR YOLO11W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN
RP SEQUENCE FROM N.A.
RA Hughes B., Pohl T.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the release of fatty acids from
CC lysophospholipids.
CC -1- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC glycerophosphocholine + a fatty acid anion.
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: Belongs to the lysophospholipase family.
CC
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CC or send an email to license@isb-sib.ch).

CC EMBL; Z74753; CAA99010.1; -.
DR PIR; S66693; S66693.
DR Germline; 143433; -.
DR SGD; S0005371; P.B3.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0004622; F:lysophospholipase activity; IMP.
DR GO; GO:0006660; P:phosphatidylserine catabolism; IDA.
DR GO; GO:0030384; P:phosphoinositide metabolism; IDA.
DR InterPro; IPR002642; PLAC.
DR Pfam; PF01735; PLAC_2; 1.
DR SMART; SM00022; PLAC; 1.
KW Lipid degradation; Hydrolase; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 686
FT DOMAIN 627 643
FT CARBOHYD 56 56
FT CARBOHYD 82 82
FT CARBOHYD 129 129
FT CARBOHYD 166 166
FT CARBOHYD 221 221
FT CARBOHYD 283 283
FT CARBOHYD 313 313
FT CARBOHYD 351 351
FT CARBOHYD 495 495
FT CARBOHYD 519 519
FT CARBOHYD 547 547
FT CARBOHYD 571 571
FT CARBOHYD 588 588
FT CARBOHYD 614 614
FT SEQUENCE 686 AA; 75076 MW; 95A2DBF41BF3E20F CRC64;
SQ
Query Match 5.7%; Score 184; DB 1; Length 686;
Best Local Similarity 21.0%; Pred. No. 2.1e-06;
Matches 129; Conservative 80; Mismatches 192; Indels 214; Gaps 31;
QY 99 EQAFLSRRKQVVAALRQAL-----QLDGLQDEIPVVAIMATGGIRA 143
DB 57 ESAMLEKRNKVTSAVKDLFTRATANFSDSSVLSKLFNDGNSENLPKIAVAVSGGYRS 116
QY 144 MTSLYCOLAGLKE-----GLDCVSVITGASSTWALANL----- 179
DB 117 MUTGAGVLAAMDNRTGAYEHGGLGLOSTTVYLSGASGGLVGLTALANWTSVQDILNN 176
QY 180 ---YEDPEWSQD---LAGTELLKTQVTKNKL-GVLAPSOLOQRYOELAE---RAELGYP 230
DB 177 MQNDDSIWLSDSIVTPGGINIFKTAKRWDHISNAVESKQADYNTSLADIWGRA-LAY- 234
QY 231 SCFTNLWALINE-----ALLHDEPHDKLSQDREALSHGQNPPIYCA---LNTKGQ 279
DB 235 ---NFFPSLNRGGIGLTWSSIRDFP-----VFQNAEMPFFISVADGRYPGKTVI 280
QY 280 SLTTFEFGWCCEFSFVEYGF--PKYGAFIPSELFGSEFFMGQMKR---LPESRICFLE 333
DB 281 NLNATVF---ENPEMGSWOPSLNSFANVKYLGTVNSGVPLERKGTAGDAGFIM 336
QY 334 GWSNLYAANLQDSLYWASEPSPQFWRWRNQNANLQDKBQVPLKIEEP---PSTAGRIA-- 389
DB 337 GTSSTLTF-----NQF-----LLRINSTHLPSTITLARH 365
QY 390 -----EFTDILLTWRLAQATHNRLGLHFKDYFQHPHSTWKTATLGLPNQTPSE 443
DB 366 FLKDLSDQDFNDIAVYSPNPKDTKFL-----DSDY-----TT-----SIVSDS 403
QY 444 PHLCLLDVGY-LINTSCLPLLOTRDVLTLSDYN-----LHGAFAQLQLL 489
DB 404 -SLFLVDGGEDDENVPVPLIQKERDVIIFAVDNSADMRLEAWPDGSSLVHYTERQVVKQ 462
QY 490 GRFCQEQIGIPFPISPSPEEQLOPRECHTF-----SDPTCPGA-----PAVL 531
DB 463 G-----QGMSPFYPV-----DTNTFNLGLNKKPTFFGCDANLTLQVIPPV 507
QY 532 HFSSGVRRTEEEAAAGEVNLSSDSPVHYTKVTYSQED-----VDKLLHLTHYNNCNOEQ 587

```

CC      coding nucleotide sequence.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to licenses@isb-sib.ch).
CC -----
CC ENBL; UI4567; -; NOT ANNOTATED_CDS.
CC -----
DR      DR          KW      Hypothetical protein_
FT      FT          1       FRAME-1.
FT      FT          100     FRAME-2.
FT      FT          199     FRAME-3.
FT      FT          298     FRAME-4.
FT      FT          397     FRAME-5.
FT      FT          496     FRAME-6.
SQ      SQ          SEQUENCE 591 AA; 63790 MW; 665D395735519D95 CRC64;

Query Match           5.6%; Score 182; DB 1; Length 591;
Best Local Similarity 81.8%; Pred. No. 2.5e-06;
Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      40 FPEMESLSVAQAGVQWRDLGSLQPPLPGFKRFSCLSLPSSWDYR 83
      |||
DB      496 FPETGSRSAQAGVQWRDHGSLQPRPPGLKRSCLSLPSSWDYR 539

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2004, 18:51:24 ; Search time 120.193 Seconds
(without alignments)
1588.179 Million cell updates/sec

Title: US-09-830-321A-2

Perfect score: 3235

Sequence: 1 MIFVESPTLALCLERVASH.....EQLLEALROAVRRQRREH 605

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2767.5	85.5	1012	4 Q9UKV7	Q9ukv7 homo sapien
2	2767.5	85.5	1012	4 Q95712	Q95712 homo sapien
3	1931.5	59.7	439	11 Q80VV8	Q80vv8 mus musculus
4	1492	46.1	818	4 Q86XP0	Q86xp0 homo sapien
5	1141.5	35.3	845	4 Q8IUP3	Q8iup3 homo sapien
6	1127	34.8	841	11 Q80VV9	Q80vv9 mus musculus
7	708	21.9	356	11 Q8BX44	Q8bx44 mus musculus
8	685	21.2	372	11 Q80V08	Q80vq8 mus musculus
9	639.5	19.8	748	6 Q8TT38	Q8tt38 oryctolagus
10	622	19.2	749	13 Q7T079	Q7t0t9 xenopus lae
11	595.5	18.5	740	11 Q9DBX5	Q9dbx5 mus musculus
12	498.5	15.4	541	4 Q8UP65	Q8up65 homo sapien
13	490.5	15.2	541	4 Q75457	Q75457 homo sapien
14	397.5	12.3	216	4 Q8N176	Q8n176 homo sapien
15	371.5	11.5	530	11 Q7TN01	Q7tn01 mus musculus
16	239	7.4	634	3 Q9F8L1	Q9p8l1 cryptococcus

17	227.5	7.0	637	3	Q9P8P2	Q9p8p2 cryptococcus
18	227	7.0	634	3	Q8X0Z4	Q8x0z4 cryptococcus
19	225	7.0	634	3	Q8WMC5	Q8wmc5 homo sapien
20	221	6.8	634	3	Q96WX0	Q96wx0 cryptococcus
21	211	6.5	157	4	Q8N845	Q8n845 homo sapien
22	205	6.3	163	4	Q96MM0	Q96mm0 homo sapien
23	200	6.2	135	6	Q95XE1	Q95kel macaca fasc
24	199	6.2	158	4	Q8NAL9	Q8nal9 homo sapien
25	198	6.1	61	4	Q9UI48	Q9ui48 homo sapien
26	196.5	6.1	138	4	Q8N874	Q8n874 homo sapien
27	194.5	6.0	162	4	Q9H5D5	Q9h5d5 homo sapien
28	194	6.0	86	4	Q8N5B5	Q8n5b5 homo sapien
29	192	5.9	122	6	Q9BGM3	Q9bgm3 macaca fasc
30	192	5.9	152	4	Q9NX85	Q9nx85 homo sapien
31	190.5	5.9	151	4	Q9HA67	Q9ha67 homo sapien
32	187	5.8	208	4	Q9NM14	Q9nm14 homo sapien
33	185	5.7	101	4	Q7Z4P3	Q7z4p3 homo sapien
34	185	5.7	375	4	Q60448	Q60448 homo sapien
35	184.5	5.7	35	4	Q8N7M7	Q8n7m7 homo sapien
36	183	5.7	180	4	Q7Z8L3	Q7z8l3 pichia jadi
37	182	5.6	162	4	Q9BYA5	Q9bya5 homo sapien
38	178.5	5.5	66	4	Q96HL9	Q96hl9 homo sapien
39	177	5.5	125	4	Q9H842	Q9h842 homo sapien
40	176	5.4	118	4	Q9H387	Q9h387 homo sapien
41	175.5	5.4	164	4	Q9UQD6	Q9uqd6 homo sapien
42	175	5.4	244	4	Q9H700	Q9h700 homo sapien
43	175	5.4	434	4	Q8N2I3	Q8n2i3 homo sapien
44	175	5.4	506	4	Q9H6L7	Q9h6l7 homo sapien
45	174	5.4	126	4	Q8N1G7	Q8n1g7 homo sapien

ALIGNMENTS

RESULT 1

Q9UKV7 PRELIMINARY; PRT; 1012 AA.
AC Q9UKV7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Cytosolic phospholipase A2 beta.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99287906; PubMed=10358058;
RA Song C., Chang X.J., Bean K.M., Proia M.S., Knopf J.L., Kriz R.W.;
RT "Molecular characterization of cytosolic phospholipase A2-beta.;"
RL J. Biol. Chem. 274:17063-17067(1999)
CC -|- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; AF121908; AAD32135.1; -;
DR HSP; P04410; 1A25.
DR GO; GO:0004620; P:phospholipase activity; IEA.
DR GO; GO:0009395; P:phospholipid catabolism; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2 CalB.
DR InterPro; IPR002642; PLAc.
DR InterPro; IPR003347; TF_JmjC.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF01735; PLA2_B; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00558; JmjC; 1.
DR SMART; SM00022; PLAc; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
SQ SEQUENCE 1012 AA; 114154 MW; 1A9D3269BA457797 CRC64;

Query Match 85.5%; Score 2767.5; DB 4; Length 1012;
Best Local Similarity 87.6%; Pred. No. 6.4e-231;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

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QY 24 TGLLVLCFPCPCPFPPFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSPSSWDYR 83
DB 418 TGTFRFHCPA-C-----WEQE-LSI-----RLQDAPEQLKAPLSALPSGGQVVR 459
QY 84 -----LRELAVRLGFGCAEQAFLSRRKQVVAAALRQALQDGD 123
DB 460 LVFPTSQEPMLMRVBLKEAGLRELAVRLGFGCAEQAFLSRRKQVVAAALRQALQDGD 519
QY 124 LOEDEIPVVAIMATGGGIRAMTSYLGQLAGLKEGLDCVSYITGASGSTWALANLYBDP 183
DB 520 LOEDEIPVVAIMATGGGIRAMTSYLGQLAGLKEGLDCVSYITGASGSTWALANLYBDP 579
QY 184 EWSQKDLAGPTTELLKTQVTKNKLGVLAAPSOLQRYQELAEARLGYPCSCFTNLWALINEA 243
DB 580 EWSQKDLAGPTTELLKTQVTKNKLGVLAAPSOLQRYQELAEARLGYPCSCFTNLWALINEA 639
QY 244 LLHDEPHDKLSQDREALSHGQNPPIYCALNTKGSLTTFEFGWCFCFSFYEVGFPKYG 303
DB 640 LLHDEPHDKLSQDREALSHGQNPPIYCALNTKGSLTTFEFGWCFCFSFYEVGFPKYG 699
QY 304 AFIPSELFGSFFFMQMLKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDWRVR 363
DB 700 AFIPSELFGSFFFMQMLKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDWRVR 759
QY 364 NQANLDKEQVPLKLTIEPPSTAGRIAEFTDILLTWRLPAQAATHNFIHGLHFKDYFOHPH 423
DB 760 NQANLDKEQVPLKLTIEPPSTAGRIAEFTDILLTWRLPAQAATHNFIHGLHFKDYFOHPH 819
QY 424 FSTWKATTLGDLNPQLTSPSEPHCLLDVGYLINTSCLPLQPTRDVDLILSLDYNLHGAF 483
DB 820 FSTWKATTLGDLNPQLTSPSEPHCLLDVGYLINTSCLPLQPTRDVDLILSLDYNLHGAF 879
QY 484 QQLQLLGRFCQBGIPFPPIPSPEQLOPRECHTFSDPTCPGAPAVLHF-----533
DB 880 QQLQLLGRFCQBGIPFPPIPSPEQLOPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 939
QY 534 -SSGVRRTPEAAAGEVNLSSDSPHYHTKVTSQEDVDKLLHLYNNVNNQOEQLLEAL 592
DB 940 SAPGVRRTPEAAAGEVNLSSDSPHYHTKVTSQEDVDKLLHLYNNVNNQOEQLLEAL 999
QY 593 ROAVQRRRRRPH 605
DB 1000 ROAVQRRRRRPH 1012

RESULT 2
O95712 PRELIMINARY; PRT; 1012 AA.
AC O95712;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Cytosolic phospholipase A2 beta.
GN CPLA2 BETA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99185108; PubMed=10085124;
RA Pickard R.T., Striffler B.A., Kramer R.M., Sharp J.D.;
RT "Molecular cloning of two new human paralogs of 85-Kda cytosolic
RT phospholipase A2.";
RL J. Biol. Chem. 274:8823-8831 (1999).
CC -I- SIMILARITY: CONTAINS 1 C2 DOMAIN.
EMBL: AF065215; AAC78836.1; -.
DR HSP; P04410; IAA25.
DR Gnew; HGNC:9036; PLA2G4B.
DR GO; GO:0004627; F:calcium-dependent cytosolic phospholipase A. . .; TAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2 CaLB.
DR InterPro; IPR002642; PLAC.

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DR InterPro; IPR003347; TF_JmJC.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF01735; PLA2_B; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00558; JmJC; 1.
DR SMART; SM00022; PLAC; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
SQ SEQUENCE 1012 AA; 114120 MW; 989EDB4AD3CF19DD CRC64;

Query Match 85.5%; Score 2767.5; DB 4; Length 1012;
Best Local Similarity 87.6%; Pred. No. 6.4e-231;
Matches 537; Conservative 5; Mismatches 22; Indels 49; Gaps 6;

QY 24 TGLLVLCFPCPCPFPPFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSPSSWDYR 83
DB 418 TGTFRFHCPA-C-----WEQE-LSI-----RLQDAPEQLKAPLSALPSGGQVVR 459
QY 84 -----LRELAVRLGFGCAEQAFLSRRKQVVAAALRQALQDGD 123
DB 460 LVFPTSQEPMLMRVBLKEAGLRELAVRLGFGCAEQAFLSRRKQVVAAALRQALQDGD 519
QY 124 LOEDEIPVVAIMATGGGIRAMTSYLGQLAGLKEGLDCVSYITGASGSTWALANLYBDP 183
DB 520 LOEDEIPVVAIMATGGGIRAMTSYLGQLAGLKEGLDCVSYITGASGSTWALANLYBDP 579
QY 184 EWSQKDLAGPTTELLKTQVTKNKLGVLAAPSOLQRYQELAEARLGYPCSCFTNLWALINEA 243
DB 580 EWSQKDLAGPTTELLKTQVTKNKLGVLAAPSOLQRYQELAEARLGYPCSCFTNLWALINEA 639
QY 244 LLHDEPHDKLSQDREALSHGQNPPIYCALNTKGSLTTFEFGWCFCFSFYEVGFPKYG 303
DB 640 LLHDEPHDKLSQDREALSHGQNPPIYCALNTKGSLTTFEFGWCFCFSFYEVGFPKYG 699
QY 304 AFIPSELFGSFFFMQMLKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDWRVR 363
DB 700 AFIPSELFGSFFFMQMLKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDWRVR 759
QY 364 NQANLDKEQVPLKLTIEPPSTAGRIAEFTDILLTWRLPAQAATHNFIHGLHFKDYFOHPH 423
DB 760 NQANLDKEQVPLKLTIEPPSTAGRIAEFTDILLTWRLPAQAATHNFIHGLHFKDYFOHPH 819
QY 424 FSTWKATTLGDLNPQLTSPSEPHCLLDVGYLINTSCLPLQPTRDVDLILSLDYNLHGAF 483
DB 820 FSTWKATTLGDLNPQLTSPSEPHCLLDVGYLINTSCLPLQPTRDVDLILSLDYNLHGAF 879
QY 484 QQLQLLGRFCQBGIPFPPIPSPEQLOPRECHTFSDPTCPGAPAVLHF-----533
DB 880 QQLQLLGRFCQBGIPFPPIPSPEQLOPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 939
QY 534 -SSGVRRTPEAAAGEVNLSSDSPHYHTKVTSQEDVDKLLHLYNNVNNQOEQLLEAL 592
DB 940 SAPGVRRTPEAAAGEVNLSSDSPHYHTKVTSQEDVDKLLHLYNNVNNQOEQLLEAL 999
QY 593 ROAVQRRRRRPH 605
DB 1000 ROAVQRRRRRPH 1012

RESULT 3
O95712 PRELIMINARY; PRT; 439 AA.
AC O95712;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Similar to phospholipase A2, group IVB (Cytosolic) (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Salivary gland;

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RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042758; AAH42758.1; -.
DR PIR; PT0721; PT0721.
DR GO; GO:0004620; P:phospholipase activity; IEA.
DR GO; GO:0009395; P:phospholipid catabolism; IEA.
DR InterPro; IPR002642; PLAC.
DR Pfam; PF01735; PLA2_B; 1.
FT NON TER 1
SQ SEQUENCE 439 AA; 50464 MW; EA9041FA820F5F10 CRC64;

Query Match 59.78; Score 1931.5; DB 11; Length 439;
Best Local Similarity 82.54; Pred. No. 6.9e-159;
Matches 358; Conservative 30; Mismatches 35; Indels 11; Gaps 1;

QY 181 EDPEWQKDLGTELLKTQVTKNKLGVLAAPSOLQRYQELARARLYGSPCTNLWALI 240
Db 1 EDPEWQKDLGTEVLKTVTKSKLGALAPSOLWRYQELARARLYGHTCTCNWALI 60
QY 241 NEALLHDEPHDKLSQREALSQGNPLPIYCALNTKGQSLTTFEGWCEFSYEVGPP 300
Db 61 NEALLHDKPEHKLSQREALSQGNPLPIYCALNSKEQSLTFEGWCEFSYEVGPP 120
QY 301 KYGARTPELFGSEFMGQMKELPESRICFLEGIWSNLVAANLQSLYWASEPQFWR 360
Db 121 KYGARTPELFGSEFMGRLVKQLPESRICFLEGIWSNLFAASLQSLYWSSEPSQFWR 180
QY 361 WVRNQNLDKEQVPLKIEPPSTAGRIAEFFDILLTWPLAQATHNGLRGLHFKDYQ 420
Db 181 WAQDQANLDEQVPLKIAEPPTMAGRIAEFFDILLTKPLAHATHNTRGLHFKDYQ 240
QY 421 HPHFSTWKAATLDGLPNQTPSEPHCLLDVGYLINTSLCLPLQTPRDVLDLILSLDYNLH 480
Db 241 NSHFSAWKASKLRLPNQLTPAEPLCLLDVGYFINTSCPPELLQTPRDVLDLILSLDYNLY 300
QY 481 GAFQQLLGRFCQEGIPFPISPSPELOQPRECHTSDPTCPGAPAVLHF 533
Db 301 GAFQQLLGRFCQEGIPFPISPSPELOQPRECHTSDPTCPGAPAVLHF 360
QY 534 ----SSGVARTPEEAAGVNLSSDSPHYTKVTSQSDVDKLLHLYNNVNNQEQLL 589
Db 361 QDYSAPGVPTSEKKAAGEVNLSSDSPHYTKVTSQSDVDKLLHLYNNVNNQEQRLR 420
QY 590 EALRQAVQRRRR 603
Db 421 EAMHQAVQRRRRK 434

RESULT 4
Q86XP0 PRELIMINARY; PRT; 818 AA.
ID Q86XP0
AC Q86XP0;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Cytosolic phospholipase A2 delta.
GN PLA2 DELTA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RA Imai Y.; Chiba H.;
RT "cytosolic phospholipase A2 homolog (cPLA2delta).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB090876; BAC7158.1; -.
DR GO; GO:0004620; P:phospholipase activity; IEA.
DR GO; GO:0009395; P:phospholipid catabolism; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.
DR InterPro; IPR002642; PLAC.
DR Pfam; PF00168; C2; 1.

DR Pfam; PF01735; PLA2_B; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00022; PLAC; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
SQ SEQUENCE 818 AA; 91955 MW; E5ADF3478FDAB180 CRC64;
Query Match 46.14; Score 1492; DB 4; Length 818;
Best Local Similarity 51.64; Pred. No. 2.6e-120;
Matches 296; Conservative 92; Mismatches 152; Indels 34; Gaps 8;
QY 61 LQPEPLGFKRFSCLSPSSWDYRLR-----ELAVRLGFGPCAEQAFLSRKQVAA 112
Db 244 LRPLTIGKEVTMDVPAPNPGVQLQKAECPPELAVHLGNLCABEQAFSLRRKQVAK 303
QY 113 ALRQALQDLQDEDEIPVVAIMATGGIRAMTSLYGQLAGLKGELGLDCVSYITGASGS 172
Db 304 ALKQALQLDRDLQDEDEVPVVGIMATGGARAMTSLYGHLLALQKGLDCCVTFYFSGISGS 363
QY 173 TWALANLYEDPEWSOKDLAGPTELLKTQVTKNKLGVLAAPSOLQRYQELARARLYGSPCT 232
Db 364 TWTMAHLYGDPEWSQDRDLGPIRYAREHLAKSKLEVFSPERLASYRRELELRAEQGHPTT 423
QY 233 FTMWALINEALLHDEPHDKLSQREALSQGNPLPIYCALNTKGQSLTTFEGWCEFS 292
Db 424 FVDLWALVLESLHGGVMDQKLSQQAALRGONPLPLVLSLNVKNNLETLLDFKEWVEF 483
QY 293 SPYEVGFPYKGAFTPELFGSEFMGQMKELPESRICFLEGIWSNLVAANLQSLYWAS 352
Db 484 SPYEVGFLYKGAFTPELFGSEFMGRLMRRIPRIPRIFLEAIWSNIFSLNLLDAMVDLT 543
QY 353 EFSQFQDRWRNQA-NLDKEQVPLL-----KLEE---PPSTAGRIAEFTDILLTWPLA 402
Db 544 SGSEWQKIKOKTKRSLEKE--PLTSGTSSKLEASWLOQGT--LAQAFKGLTGRPLH 599
QY 403 QATHNPLRGLHFKDYFQHPHFSTWKAATLDGLPNQTPSEPHCLLDVGYLINTSLCLPL 462
Db 600 ORSPNPLQGLQHQDYCSHKDFSTWADYQDMSFSLTKPEPLCLVDAAYFINTSSPSM 659
QY 463 LQPTRDVLDLILSLDYNLHGAFOQLQLLGRFCQEGIPFPISPSPELOQPRECHTFSDF 522
Db 660 FRPGRRLDILSFDYSLSAPEALQOTELYCRARGLPFRVPSPDQHQPRECHLFSDF 719
QY 523 TCGAPAVLHF-----SSGVARTPEEAAGVNLSSDSPHYTKVTSQSDVDKLLHLYNNV 571
Db 720 ACPEAPILLHPLVNASFKDHSAPGVQSPAPLQSGQVDLTGATCPYTLNNTYKEEDFE 779
QY 572 KLLHLTHYNNVNNQEQLLLEALRQAVQRRR-ORRP 604
Db 780 RLRLSDYNNVQTSQGAILLQALRTALKHRTLEARP 813

RESULT 5
Q8IUP3 PRELIMINARY; PRT; 845 AA.
ID Q8IUP3
AC Q8IUP3;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Similar to phospholipase A2, group IVB (Cytosolic) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035335; AAH35335.1; -.
DR GO; GO:0004620; P:phospholipase activity; IEA.
DR GO; GO:0009395; P:phospholipid catabolism; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.


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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).
DR EMBL; AK049063; BAC33531.1;
DR GO; GO:0004620; F:phospholipase activity; IEA.
DR GO; GO:0009395; P:phospholipid catabolism; IEA.
DR InterPro; IPR002642; PLAC.
DR Pfam; PF01735; PLA2_B; 1.
DR SMART; SM00022; PLAC; 1.
DR Hypothetical protein.
SQ SEQUENCE 356 AA; 40682 MW; 5968D5518E290FEB CRC64;

Query Match 21.9%; Score 708; DB 11; Length 356;
Best Local Similarity 49.2%; Pred. No. 8.6e-53;
Matches 145; Conservative 43; Mismatches 81; Indels 26; Gaps 4;

QY 72 SCLS-----LPSWDYRLR-----ELAVLGFPCAEQAFUSRRKQVVAALRQA 117
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
65 NCLSDGQVTLTPGVENYELMKSSPCSDTLVRLGFSLCOEEVEFVQKRKMVAKTLSQM 124
QY 118 LQLDGDIDQEDIPVVAIMATGGGIRAMTSLYGOLAGLKLGLDVCYSYITGASGWTALA 177
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
125 LQLEGLHEDVEPIIAMATGGGTRSMVSLYGHLLQKLNFLDASTYITGLSGATWMA 184
QY 178 NLYDEPWSOKDLAGPTELLKTOVTKNKLGVLAFLPSQLQRYQBLAERARLGYSCFTNLW 237
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
185 TLYSDPEWSKNLETVVFEARRHWKXMPALFPDQLYKWRDLQKHSQEGYKTTDFW 244
QY 238 ALINEALLHDEPHDKLSDOREALSHGONPLPYCALNTKGSLTFTEFGWCFFSPYEV 297
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
245 KGLIEYSLGDKNECKLSQRAALCKGQNPPLTYLTINVK-DDVSNQDFREWFSPYEV 303
QY 298 GFPKYGAFIPSELFSGEFFGQMLKRLPESRICFLGINSWLNVAANLQDSLYWAS 352
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
304 GMQKYGAFIPSELFSGEFFGQMLKRLPESRICFLGINSWLNVAANLQDSLYWAS 352
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 8
Q80VQ8 PRELIMINARY; PRT; 372 AA.
AC Q80VQ8
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to phospholipase A2 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Breast tumor;
RX Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046400; AAH46400.1;
DR GO; GO:0004620; F:phospholipase activity; IEA.
DR GO; GO:0009395; P:phospholipid catabolism; IEA.
DR InterPro; IPR002642; PLAC.
DR Pfam; PF01735; PLA2_B; 1.
DR NON_TER 1
FT
SQ SEQUENCE 372 AA; 42638 MW; 17BD15B59207A8BC CRC64;

Query Match 21.2%; Score 685; DB 11; Length 372;
Best Local Similarity 39.5%; Pred. No. 9.1e-51;
Matches 145; Conservative 68; Mismatches 126; Indels 28; Gaps 7;

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QY 261 LSHQONPLPYCALNTKGSLTFTEFGWCFFSPYEVGFPKYGAFIPSELFSGEFFMGQL 320
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 VSQONPYPIYASINVH-KNISGDYFAEWCEFTYEVGFPKYGVVPTTELFSGEFFMGRL 59
QY 321 MKRLPESRICFLGINSWLNVAANLQDSLYWASPSQFWDWRVNRQANLQDSQVLLKIEE 380
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
60 LHPFEPERICVQMGWSAFAASLYEFLKLGSLSLFLDWHRGVSFV-TDDWPKLRQD 118
QY 381 PPSTAGRI-----ABFDTLLTWRELAQATHNFLRGLHFKHDYFQHPHF-----STWKA 429
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
119 PTRLPTLFTPMSSFSQAVLDIFTSRTCAQTFNTRGLCMYKDYTARKDPVSEDAWHS 178
QY 430 TTL---DGLPNOLTPSEPHCLLDVGYLINTSCPLLOPTRDVLILSLDNLHGAFOQL 486
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
179 HNYGYPDACPQNLTQPMKDFLSVDGGFAINSFPFLVLPQRAVDLIVSFYSLEGPFVL 238
QY 487 QLLGRFCQEOGIPFPPIPSPEQLQPRCHTSDPTCPGAPAVLHF-----SS 535
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
239 QVTEKYCRDRGIPFPRLEVDPKDSDPRECYLTFEADPCSPVLHPLVNRTRTHLAP 298
QY 536 GV-RRTEEAAGENVNLSSDSPYHYTKVTSQEDVDKLLHLTHYVNCNNOQLLEALRQ 594
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
299 GVERQTAEEKAFGDFIINGPDTAVGMMDFTYEPKEFDRLVTLRYNVLNKKETIRHALQL 359
QY 595 AVORRRQ 601
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
359 ALDRRRQ 365

RESULT 9
Q9TT38 PRELIMINARY; PRT; 748 AA.
ID Q9TT38
AC Q9TT38
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phosphatidyl choline 2-acylhydrolase cPLA2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand White; TISSUE=Heart;
RX Al-Khalili O.K.; Eaton D.C.;
RL "Molecular cloning of cDNA coding for phospholipase A2.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; AF204923; AAF15299.1; -.
DR HSSP; P47712; 1BC1.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004620; F:phospholipase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0009395; P:phospholipid catabolism; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.
DR InterPro; IPR000209; Peptidase_S8.
DR InterPro; IPR002642; PLAC.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF01735; PLA2_B; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00022; PLAC; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
DR Hydrolase.
SQ SEQUENCE 748 AA; 85235 MW; 7661A3EFC41FF668 CRC64;

Query Match 19.8%; Score 639.5; DB 6; Length 748;
Best Local Similarity 28.1%; Pred. No. 2.4e-46;
Matches 181; Conservative 118; Mismatches 237; Indels 107; Gaps 22;

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QY 44 ESLSVAQGVQWRDLGSLQPPPLGFKRPS-----CULSPSSWDYRLRELAVRLGFGPCA 97

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Db 100 ETLCATPTSSMKVGGKKEVPFFNFQVTEMLMSLEVCSPPD-----LRFSMALCD 152
QY 98 EEOAFLSRKQVAAALRQAL---OLGDLOEDBIPVVAIMATGGIRAMTSLYGQLAGL 154
Db 153 QEKAFRQQRKENIKENMRKLLGPKKSEGLYSTRDVPVVAILGSGGFRAMVGFSGVMKAL 212
QY 155 KELGLDCVSVITGASSTWALANLYDEPWSOKDLAPTEL---LKTQVTKNKLGVLP 211
Db 213 YESGILDCAITYAGLSSTWNTSLYSHDPPEK---GPQENBELMKVNSHNPLLLTTP 269
QY 212 SOLQRYRELAERARLGVSPCFNLWA-LINEALLHDEPHDKLSQDREALSHGNPLPI 270
Db 270 QKRYKVESLWKXSSGQPVFTDFGLMIGETLHNRMHT-TLSSLKEKVSSAQCPLPL 328
QY 271 YCALNTKQSLTTFEFGWCSPSPYEVGPKYGAIPSELFGSEFFMGQLMKRLPESRIC 330
Db 329 FTCLHVK-PDVSSELMAFWDFSPYEGIMAKYGTMAPDLFGSKFFMGTVVKYBENPLH 387
QY 331 FLEGIWSNLYAANLQDSLYWASEPQFWDWRVNRQANLDKEOVPLL----- 376
Db 388 FLMGVWGSFSLFNRVLGVSGS-----HNKGSITWEELEENITAXHIVNSDSDSD 438
QY 377 -KIEPPPTAGRIA--EFTD-LLTW--RPL-----AQATHNFLRGLHF 414
Db 439 DESQEPKGTGEDAEREYQNDHQASVHMLMALVSDSALFNTRREGRAKGVHFMGLNL 498
QY 415 HKDY-----FOHPHFTWKAATLIDGLPNQ-----LTPSEPHCLLDVGYLINTSCL 460
Db 499 NTSYPLSPURDFTQESFDDDELDAADVADPEFERIYEPDLVKSKKIHVVDSGLTFNLVYP 558
QY 461 PILQPTRDVLDLILSDYNLHGA-----FOLOLGRFCOEQGIPIPPISPEEQLOPRE 515
Db 559 LILRQGRVDLIIISDFSRPDSPTSPFKELLAEKWKANKLPFKPIDPYVFDREGLKE 618
QY 516 CHTFSDPTCP---GAPAVLHF-----SSGV-RRTPEEAAAGVNL-SSSDSPY 558
Db 619 CVVFK-PKNPDVEKDCPIIIHFVLANINFRKYKPGVPRETKKEIBADFDIPDDPSFP 677
QY 559 HYTKVTSQEDVDKLLHLTHYVNNQOEQLLEALROAVQRRQ 601
Db 678 STNFQYPNQAFKRLHLMFYNTLNNIDVIKIDAMVESIEYRRQ 720
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RESULT 10

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Q770T9 ID PRELIMINARY; PRT; 749 AA.
AC Q770T9;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056041; AAH56041.1;
KW Hypothetical protein.
SQ SEQUENCE 749 AA; 85282 MW; CE769904144C4DE2 CRC64;

Query Match 19.2%; Score 622; DB 13; Length 749;
Best Local Similarity 27.6%; Pred. No. 7.9e-45;
Matches 177; Conservative 113; Mismatches 219; Indels 132; Gaps 22;

QY 59 GSLQPPPLGFKRFS-----CLSLPSSWDYRLRELAVRLGFGCAEEQAFLSRRKQVAA 112
Db 115 GEKKQVPPTFNKVTMELFEFSLEVCSTD-----LRFSMALCDEKLPQKRNKVIN 167
QY 113 ALRQAL--QLDGLQED--EIPVVAIMATGGIRAMTSLYGOLAGLKEGLDCVSYITG 168
Db 168 GLRKLGLPKTQDLNSTSDVPIAVLGGGGFRAMVGFSGVMKALYESGLDCATVAG 227
QY 169 ASGSTWALANLYDEPWSOKDLAPTEL---LKTQVTKNKLGVLAISOIQRQELAE 225
Db 228 LSGSTWYMTSLYSHDPDFTK---GPKEINKELMHNVSYNPLLLLTQPKYRYVEALWKK 284
QY 226 RLGYPCFNLWA-LINEALLHDEPHDKLSQDREALSHGNPLTYCALNTKQSLTTF 284
Db 285 SSGQPVPTFDIFAMLIGETLIDR-MNRKLSHMQEKINDGQCDPLFTCLHVK-PDVS 342
QY 285 EFGWCEFSYEVGPKYGAIPSELFGSEFFMGQLMKRLPESRICFLEGINSLNLAANL 344
Db 343 MFADWTFEFSYELGMAYKGTFFMPGLFGSKFFMGTVKKYEENPLHFFMGVWGSFSLI 402
QY 345 QDSLYWASEPQFWDWRVNRQANLDKEOVPLLK-----IEEPSTAGRIA 389
Db 403 NRVLGVSN-----NSKGSMTBEEIEENLKPHEILGNDSDDSDDEMQEPKGTENAKA 452
QY 390 E---FTDLLTW--RPL-----AQATHNFLRGLHFKDYFOHPHFTW 428
Db 453 EEEYLRNQASVWQRMMLAILGDSALFNTRREGRAKGVHFMGLNLTNSYPSF----- 506
QY 429 ATTLDGLPNQLTPSEPHL-----CLLDVGYLINTSCLPLLQ 464
Db 507 ---LSGLCTQOSMEEDLDAADPDEFEQIYEPLDVSKKIHIVDSGLTNLPYLILR 563
QY 465 PTDVDLILSDYNLHGA-----FOLOLGRFCOEQGIPIPPISPEEQLOPRECHTF 519
Db 564 PQRGVDLIIISDFSRPDSPTSPFKELLAEKWKANKLPFKPIDHVFDRGLKECYIF 623
QY 520 S-----DPTCPGAPVLFH-----SSGV-RRTPEEAAAGVNL-SSSDSPY 560
Db 624 KPNKTSVEKDC---PTVIHFVLANLQPNFKAPGVPRETTEESADFDIPDDPTPST 680
QY 561 TKVTSQEDVDKLLHLTHYVNNQOEQLLEALROAVQRRQ 601
Db 681 ENFQYPNVAFKQLHLMFEFNTLNNIVKQAMVESIEYRRQ 721
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Db 70 GLLDAVYTLVAGVSGTWAISLYTNDGMEALD-----LKHRTFQEW-----DL 116
QY 215 QRYQELAEARLGYSPCFNLWA-LINEALLHDEPHDKLSDOREALSHGONPLIYCA 273
Db 117 AKSLQKTIQAARSENYS-LTDFWAMVWISKQTRRELPESH-LSNMKKPVVEGTLPYPIFAA 174
QY 274 ---LNTKGSLTTFEGCEWCFSEYVGFYKYGAFIPSELSFGSEFFMGOLMKRLPESRI 329
Db 175 IDNDLQPSWQARAPD--TWFEFTPHAGFALGAFVSI THFGSKFKKGRIVRTHPERDL 232
QY 330 CFLEGINW-----LYA--ANLQDSLY 349
Db 233 TFLRLWGSALGNTVIREYIFDQLNLTKLWRRVANAKSIGHLIFARLLRQESSQ 292
QY 350 W-----ASEPSQFW-----DRWRNOANLDEQVLLKTEBPPSTAGRIAEFF----- 392
Db 293 GEHPPPEDEGGEPEHTWLTMLENTR--TSLEKOEQ-----HEDPERKGSLSNLMDFVK 346
QY 393 -TDLLTWPLAQATHNRLGLHFKDYFQHPHFSTWKATTLTDLGLNQLTSPSEPHCLLDV 451
Db 347 KTGICASKWEGWTTNHL-----YKH-----GGIRDKIMSSRKHLHLVDA 386
QY 452 GYLINTSCLPLLOPTRDNDLILSLDYNLHGAFQQLLGRFCQEQI PPPPIPSPEEQ 511
Db 387 GLAINTPPLVLPPTREVHLLILSDFESAGDPETIRATTDYCRHKIPPPQVE---EABL 443
QY 512 Q-----PRECHTFSPTCPGAPAVLHFFSSGVRTP---EAAAGEVNLSSDSPHYTKV 563
Db 444 DLWSKAPASCYILKGET---GPVWHF-----PLFNIDACGGDIEAWSDTYD7FKLAD 493
QY 564 TYSQEDVDKLLHLYTHVNCNOEQLEAL 592
Db 494 TYTLDVVLLALAKKNVRENKKILREL 522

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RESULT 13

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O75457 PRELIMINARY; PRT; 541 AA.
ID O75457;
AC O75457;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytosolic phospholipase A2-gamma.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98371032; PubMed=9705332;
RA Underwood K.W., Song C., Kriz R.W., Chang X.J., Knopf J.L., Lin L.L.;
RT "A novel calcium-independent phospholipase A2, cPLA2-gamma, that is
RL prenylated and contains homology to cPLA2.";
RT J. Biol. Chem. 273:21926-21932(1998).
DR EMBL; AF058921; AAC32823.1; -.
DR Genew; HGNC:19037; PLA2G4C.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0004628; F:calcium-independent cytosolic phospholipase. .; TAS.
DR InterPro; IPR002642; PLAC.
DR Pfam; PF01735; PLA2 B; 1.
DR SMART; SM00022; PLAC; 1.
SQ SEQUENCE 541 AA; 60920 MW; BBB972A611FB5237 CRC64;

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Query Match 15.2%; Score 490.5; DB 4; Length 541;
Best Local Similarity 27.6%; Pred. No. 1.3e-33;
Matches 157; Conservative
QY 98 EEOAFLSRRKQVVAALRQALQLDGDIQEDEIPVWATMGGGTRAMTSYLGOLAGLKL 157
Db 15 EEKAAVERRRHLVILKALKL-----RIEAEAPVAVVIGSGGGGRRAHIAICLVISEMKEQ 69

```

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QY 158 GLLDCVSYITGASGTWALANLYE---DPEWSQDKLAGPTTELLKTQVTKNKLGVLPASQL 214
Db 70 GLLDAVYTLVAGVSGTWAISLYTNDGMEALD-----LKHRTFQEW-----DL 116
QY 215 QRYQELAEARLGYSPCFNLWA-LINEALLHDEPHDKLSDOREALSHGONPLIYCA 273
Db 117 AKSLQKTIQAARSENYS-LTDFWAMVWISKQTRRELPESH-LSNMKKPVVEGTLPYPIFAA 174
QY 274 ---LNTKGSLTTFEGCEWCFSEYVGFYKYGAFIPSELSFGSEFFMGOLMKRLPESRI 329
Db 175 IDNDLQPSWQARAPD--TWFEFTPHAGFALGAFVSI THFGSKFKKGRIVRTHPERDL 232
QY 330 CFLEGINW-----LYA--ANLQDSLY 349
Db 233 TFLRLWGSALGNTVIREYIFDQLNLTKLWRRVANAKSIGHLIFARLLRQESSQ 292
QY 350 W-----ASEPSQFW-----DRWRNOANLDEQVLLKTEBPPSTAGRIAEFF----- 392
Db 293 GEHPPPEDEGGEPEHTWLTMLENTR--TSLEKOEQ-----HEDPERKGSLSNLMDFVK 346
QY 393 -TDLLTWPLAQATHNRLGLHFKDYFQHPHFSTWKATTLTDLGLNQLTSPSEPHCLLDV 451
Db 347 KTGICASKWEGWTTNHL-----YKH-----GGIRDKIMSSRKHLHLVDA 386
QY 452 GYLINTSCLPLLOPTRDNDLILSLDYNLHGAFQQLLGRFCQEQI PPPPIPSPEEQ 511
Db 387 GLAINTPPLVLPPTREVHLLILSDFESAGDPETIRATTDYCRHKIPPPQVE---EABL 443
QY 512 Q-----PRECHTFSPTCPGAPAVLHFFSSGVRTP---EAAAGEVNLSSDSPHYTKV 563
Db 444 DLWSKAPASCYILKGET---GPVWHF-----PLFNIDACGGDIEAWSDTYD7FKLAD 493
QY 564 TYSQEDVDKLLHLYTHVNCNOEQLEAL 592
Db 494 TYTLDVVLLALAKKNVRENKKILREL 522

```

RESULT 14

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O8N176 PRELIMINARY; PRT; 216 AA.
ID O8N176;
AC O8N176;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to phospholipase A2, group IVB (Cytosolic).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034571; AAH34571.1; -.
SQ SEQUENCE 216 AA; 24371 MW; 6198D0A387F1071B CRC64;

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```

Query Match 12.3%; Score 397.5; DB 4; Length 216;
Best Local Similarity 39.5%; Pred. No. 3.6e-26;
Matches 92; Conservative 37; Mismatches 75; Indels 29; Gaps 8;
QY 317 MGOLMKRLPESRICFLEGINSNLYAANLQDSLWASEPSQFWRWRWNRQA-NLDKQVPL 375
Db 1 MGRLMRRRIPEPRICFLEAIWSNIFSLNLDADWYDLTSSGSESWKOHKDKTRSEKE--PL 58
QY 376 L-----KIEE---PPSTAGRIAEFFTDLLTWPLAQATHNRLGLHFKDYFQHPHFST 425
Db 59 TTSGTSRLRLANLQCGTA--LQAQKFGTLTGRLHORSFNFLQGLHODYCSHKDFST 116
QY 427 WKATTLTDLGLPNQLTSPSEPHCLLDVGYLINTSCLPLLOPTRDNDLILSLDYNLHGAFQOL 486
Db 117 WADYQLDSMPSQLTPKEPRCLVDAAYFINTSSPSMFRPGRRLDILSFDYLSAPFE-- 174

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QY 487 QLLGRFCQGGIPFPPI-SPSPPEQIQPRECHTFSDPTCPGAPAVLHFSSGVR 538
Db 175 -----VPMSPQGNPSAQPGQAPASSRATER-LPHTARVPKRRGVR 215

RESULT 15
ID Q7TN01 PRELIMINARY; PRT; 530 AA.
AC Q7TN01;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054740; AAH54740.1;
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 530 AA; 60927 MW; 2029EA78CDBC4265 CRC64;

Query Match 11.5%; Score 371.5; DB 11; Length 530;
Best Local Similarity 24.8%; Pred. No. 2.6e-23;
Matches 135; Conservative 73; Mismatches 177; Indels 159; Gaps 20;

QY 155 KELGLLDCVYITGASGTWALNIYEDPEWSQKDLAGFTELLTKQTQVTKKLGVLAPSQL 214
Db 1 KELGLLDVTVLAGVSGSTWALSSLYT---KNGNMEGIEBELKHRYEKNEWDF----- 50

QY 215 QRYQELALERA-----RLGYSCFTNLWALINEALHDEPHDKLSQOREALSHGQNLFP 269
Db 51 ----HESLEKAIOASKRENY--SLTDFWYLVTSRQIRELQDSNLSLKKQVEGVLPYP 104

QY 270 IYCALN-----TKGSLTTPFEGWCCEFSYEVGPKYGAIPSELGSEFFMQQL 320
Db 105 IFAAIDEDLLADWRERKTON-----SWFEFPHAGYPALGAYVPIFEFSRFENGKL 157

QY 321 MKRLPESICFLEGIWSNLYANLQDSLYWASEPSQFWDWRVRNQ-ANLDEQVPLLKIE 379
Db 158 VKSEPERDLTLRLGLWSAF-ADIKE-----IKNYILNFRNPFGLKAFI 201

QY 380 EPPSTAGR-----IAEFTD-----L 395
```

```
Db 202 EGPVTYSEAPRMNVDAMLLDLWMAFYDMNDPSIKDKLCAQLQALGTETDEFGIEMAEII 261
QY 396 LTWRPL-AQATHNPL-----RGLHFHKDYFQHPH---FSTWK 428
Db 262 QNMNETSAEKKEQFLDHLDDRFRKKTQEDTTTYSLMNWNNTGLVWDRCVFVNETRKCYSKWQ 321
QY 429 ATTL-----DGLPNQLTPSEPHLCCLLDVGYLINTSCLPLOPTRDVLILSLDYNLHG 481
Db 322 WGTVYNFLYKHGKIADETWCSELHLHLVDAGFAINTFPYPLVLPVPRETHLILSDFDSAGD 381
QY 482 AFQQLQLGRFCQEQGIPFPPI-SPSPPEQIQ-----PRECHTFSDPTCPGAPAVLHF--- 533
Db 382 PLETIRATADYQCRHEIPPEVS---EDQLKEWAKAPASCYVLRGET---GPVVMETLTF 435
QY 534 ----SSGVRTPEAAAGAEVNLSSSDSPHYTKYTSQEDVDKLLHLTHYVNCNNOQLLE 590
Db 436 NKDNCGDDIETWRKKYGTVKLSDS-----YTPDLVRDLLRVSKENVKKNKINILS 485
QY 591 ALRQ 594
Db 486 EMRK 489
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Search completed: October 5, 2004, 19:24:07
Job time : 125.193 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2004, 12:49:19 ; Search time 1674.58 Seconds
(without alignments)
10556.917 Million cell updates/sec

Title: US-09-830-321A-4

Perfect score: 592

Sequence: 1 ttgtcctccactgctctgtg.....cccgagctccccggaacc 592

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	587.2	99.2	726	14	CD691591 EST81114 h
2	527.6	89.1	680	12	BI836812 603084703
3	436.4	73.7	438	29	AY417051 Homo sapi
4	436.4	73.7	438	29	AY417052 Pan trogl

5	427.2	72.2	463	12	BM153087
6	323	54.6	461	14	CB481980
7	308.6	52.1	424	14	CD687559
8	296.6	50.1	623	13	BY752231
9	296	50.0	1582	11	AK018005
10	289.8	49.0	438	29	AY417053
11	268.8	45.4	460	9	AI430241
12	268.8	45.4	501	9	AA762051
13	265.8	44.9	601	13	BQ418599
14	265.8	44.9	998	13	BY704474
15	265.8	44.9	1206	11	AK004232
16	259.8	43.9	484	12	BM106914
17	259.6	43.9	472	10	BE138146
18	252.8	42.7	629	14	CB437446
19	249.4	42.1	603	14	CB451900
20	247.4	41.8	432	10	BB850720
21	240.6	40.6	388	10	BF150826
22	234.2	39.6	367	10	BB869347
23	225	38.0	352	13	BY221065
24	219.4	37.1	359	13	BY214853
25	213.6	36.1	339	13	BY215822
26	210	35.5	558	12	BM363855
27	208	35.1	334	13	BY216497
28	201.4	34.0	360	13	BY211786
29	194	32.8	356	10	BB868695
30	192.6	32.5	340	13	BY216553
31	187	31.6	442	9	AI769633
32	179.4	30.3	392	10	AW659630
33	140.4	23.7	233	10	AW418175
34	135.6	22.9	643	14	CB453372
35	131.8	22.3	224	13	BY008213
36	124	20.9	554	29	CE203341
37	121.2	20.5	416	29	AY417601
38	119.6	20.2	417	29	AY417600
39	119.6	20.2	688	14	CK003597
40	117.4	19.8	521	10	AW660275
41	117.4	19.8	558	10	AW658438
42	117.4	19.8	567	10	AW658432
43	117.4	19.8	579	12	BI540965
44	115.8	19.6	570	12	BI975432
45	114.8	19.4	544	10	BE015249

ALIGNMENTS

RESULT 1
CD691591
LOCUS CD691591 726 bp mRNA linear EST 25-JUN-2003
DEFINITION EST81114 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD691591
VERSION CD691591.1 GI:32213459
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 726)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
1. .726
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN	
Query Match	99.2%; Score 587.2; DB 14; Length 726;
Best Local Similarity	99.5%; Pred. No. 1.8e-133;
Matches 589; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 TCTGCTCCACTGCTGTGGATCATGAACTGCACTGCTGTGTGGCTGGTGGT 60
Db	45 TCTGCTCCACTGCTGTGGATCATGAACTGCACTGCTGTGTGGCTGGTGGT 104
Qy	61 GATGCTGGTGTGATTCATCCAGGGCGGGATCTGAACTGAAACAAAGATGTCACGA 120
Db	105 GATGCTGGTGTGATTCATCCAGGGCGGGATCTGAACTGAAACAAAGATGTCACGA 164
Qy	121 AGTACTGGGAAATGCCATCTCTCTACTTGGCCCTACGCTGTCTACTGGGACTAGG 180
Db	165 AGTACTGGGAAATGCCATCTCTCTACTTGGCCCTACGCTGTCTACTGGGACTAGG 224
Qy	181 TGGCAGAGGCCAAACCAAGATGCCAGGACTGTGTGCTGCCAGACCCATGCTGTGCTA 240
Db	225 TGGCAGAGGCCAAACCAAGATGCCAGGACTGTGTGCTGCCAGACCCATGCTGTGCTA 284
Qy	241 TGACACCTGAAGACCCAGGGGTGGGCACTTACAGGACTATTACAGATACACTTTTC 300
Db	285 TGACACCTGAAGACCCAGGGGTGGGCACTTTCAGGACTATTACAGATACACTTTTC 344
Qy	301 CAGAGGGAACATCCACTGCTCTGACAGGGAAGCTGTGTGAGCAGCAGCTGTGTGCTG 360
Db	345 CAGAGGGAACATCCACTGCTCTGACAGGGAAGCTGTGTGAGCAGCAGCTGTGTGCTG 404
Qy	361 TGACAGGAGGTGGCTTCTGCTTGAAGGCCAACCCTGGACACCTTACAGAGCGACTGGC 420
Db	405 TGACAGGAGGTGGCTTCTGCTTGAAGGCCAACCCTGGACACCTTACAGAGCGACTGGC 464
Qy	421 TTTTCTACTGGCGGCCCACTGCGGGGGGAGAGCCCTGAGTGTGAGCAGCAGCCCTC 480
Db	465 TTTTCTACTGGCGGCCCACTGCGGGGGGAGAGCCCTGAGTGTGAGCAGCAGCCCTC 524
Qy	481 TACCTGTTCCTCAGCATGGAGCTGTGGATCCCACTCAGTATCTAACCTGAACAGC 540
Db	525 TACCTGTTCCTCAGCATGGAGCTGTGGATCCCACTCAGTATCTAACCTGAACAGC 584
Qy	541 CTGGCTTTTCAAACTCCGGGGGAGGTAGTCCAGCCCTCCCGGAACCC 592
Db	585 CTGGCTTTTCAAACTCCGGGGGAGGTAGTCCAGCCCTCCCGGAACCC 636

RESULT 2
BI836812 680 bp mRNA linear EST 04-OCT-2001
LOCUS 603084703F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5223912 5',
DEFINITION mRNA sequence.
ACCESSION BI836812
VERSION BI836812.1 GI:15948362
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 680)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIA011563 row: e column: 01
High quality sequence start: 4
High quality sequence stop: 680.
Location/Qualifiers
1. 680
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5223912"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC library."

ORIGIN

Query Match	89.1%; Score 527.6; DB 12; Length 680;
Best Local Similarity	98.6%; Pred. No. 7.7e-119;
Matches 574; Conservative	0; Mismatches 4; Indels 4; Gaps 4;
Qy	12 TGCTCTGTGTGGATCATGGAACCTGCACTGCTGTGGCTGTGGTGGTGGTGGTGG 71
Db	1 TGCTCTGTGTGGATCATGGAACCTGCACTGCTGTGGCTGTGGTGGTGGTGGTGG 60
Qy	72 TCATTTCCCAATCCAGGGCGGATCTTGAACCTCAACAAAGATGCTCAAGCAAGTGA 131
Db	61 TCATTTCCCAATCCA-GGGCGGATCTTGAACCTCAACAAAGATGCTCAAGCAAGTGA 119
Qy	132 AAATGCCATCTCTCTCTACTGGCCCTACGGCTGTCACTGCGGACTAGTGTGGCAGG 191
Db	120 AAATGCCATCTCTCTCTACTGGCCCTACGGCTGTCACTGCGGACTAGTGTGGCAGG 179
Qy	192 AACCCAAAGATGCCAGGACTGTGTGTCGCCAGACCATGACTGCTCTATGACCACCTGA 251
Db	180 AACCCAAAGATGCCAGGACTGTGTGTCGCCAGACCATGACTGCTCTATGACCACCTGA 239
Qy	252 AGACCCAGGGGTGGGCACTTCAAGGACTATTACAGATACAACTTTTCCAGGGGAACA 311
Db	240 AGACCCA-GGGTGCAGCATCTACAGGACTATTACAGATACAACTTTTCCAGGGGAACA 298
Qy	312 TCACCTGCTCTGACAAAGGAAAGCTGTGTGAGCAGCAGCTGTGTGCTGTGACAAGGAGG 371
Db	299 TCACCTGCTCTGACAAAGGAAAGCTGTGTGAGCAGCAGCTGTGTGCTGTGACAAGGAGG 358
Qy	372 TGGCCCTTCTGCTGAGCGCAACCTGGACACCTTACAGAGCGACTGCGTTTCTACTGGC 431
Db	359 TGGCCCTTCTGCTGAGCGCAACCTGGACACCTTACAGAGCGACTGCGTTTCTACTGGC 418
Qy	432 GGCCCCCACTGCCCGGGG-CAGACCCCTGGGTGTAGAAAGCCCAACCCCTCTACCCCTGTTTC 490
Db	419 GGCCCCCACTGCCCGGGGCGAGACCCCTGGGTGTAGAAAGCCCAACCCCTCTACCCCTGTTTC 478
Qy	491 CTCAGCATGAGCTGTGGCATGCCCACTCAGTATCTTAACCTGAACAGCCTGCTTTTC 550
Db	479 CTCAGCATGAGCTGTGGCAT-CCCACTCAGTATCTTAACCTGAACAGCCTGCTTTTC 537
Qy	551 AAACACTCCCGGGGAGGTAGTCCAGCCCTCCCGGAACCC 592
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RESULT 3
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[illegible]

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||||| 449 CAGACCCCTGGGTGCTAG 466
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||||| 421 CAGACCCCTGGGTGCTAG 438
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RESULT 5
BML153087
LOCUS
DEFINITION
  TCBAP1313560 Pediatric pre-B cell acute lymphoblastic leukemia
  Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP131356, mRNA
  sequence.
ACCESSION
  BML153087
VERSION
  BML153087.1 GI:17177919
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 463)
REFERENCE
  Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,
  Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
  Pediatric Leukemia cDNA Sequencing Project (2001)
  Unpublished (2001)
  Contact: Dr. Judith F. Margolin
  Texas Children's Cancer Center and Human Genome Sequencing Center
  at Baylor College of Medicine
  1102 Bates, MC3-3320 Houston, TX 77030, USA
  Tel: 832-824-4536
  Fax: 832-825-4038
  Email: clones@tccc.org
  Seq primer: M13 primer.
  Location/Qualifiers
    1..463
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    /clone="TCBAP131356"
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    /dev_stage="pediatric 2 years"
    /lab_host="DH10B"
    /clone_lib="pediatric pre-B cell acute lymphoblastic
    leukemia Baylor-HGSC project-TCBA"
    /note="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
    First strand cDNA was primed with an anchored
    XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGCGCGAGGAG(T)VN
    3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
    was primed with a BamHI-dC primer
    [5'AGAGACTCGATCCGCGCGCGCAATAATAAT(C) 3'].
    Double-stranded cDNA was then digested with BamHI and XhoI
    and directionally cloned into the BamHI and SalI sites of
    lambda pSB vector. Library went through one round of
    normalization. Library was constructed by Wei Yu at RIKEN
    of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
    Itoh M, Nagaoaka S, Sasakini, Okazaki Y, Muramatsu M,
    Schneider C, Hayashizaki Y, High efficiency selection of
    full-length cDNA by improved biotinylated cap trapper.,
    DNA Res 4: 1, 61-6, Feb 28, 1997)"
  ORIGIN
    source
    72.2%; Score 427.2; DB 12; Length 463;
    Query Match 99.3%; Pred. No. 2.9e-94;
    Best Local Similarity 0; Mismatches 3; Indels 0; Gaps 0;
    Matches 429; Conservative 0;

  QY 1 TCTGCTCCACTGCTGCTGGGATCATGGAACTTGCACTGCTGTGGGTGGTGGT 60
  Db 32 TCTGCTCCACTGCTGCTGCTGGGATCATGGAACTTGCACTGCTGTGGGTGGTGGT 91
  QY 61 GATGGCTGGTGTGATTCCAATCCAGGCGGGATCTCGAACCTGAACAGATGTCAGCA 120

```

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||||| 152 AGTGACTGGGAAATGCCATCTCTCTACTGTCCTTACGGCTGTCTCACTCGGACTAGG 211
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|||||
||||| 212 TGGCAGAGGCCAACCCAAAGATGCCAGGACTGTGTGTCGACACCCATGACTGTGCTA 271
|||||
||||| 241 TGACCACTGAAGACCCAGGGGTGGGCATCTTACAGGACTATTACAGATCAACTTTTC 300
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||||| 272 TGACCACTGAAGACCCAGGGGTGGGCATCTTACAGGACTATTACAGATCAACTTTTC 331
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||||| 301 CCAGGGGAACATCCACTGCTCTGACAAAGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCCTG 360
|||||
||||| 332 CCAGGGGAACATCCACTGCTCTGACAAAGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCCTG 391
|||||
||||| 361 TGACAAAGAGTGGCTTCTGCTGAAGCGCAACCTGGACACCTACAGAGCGACTGG 420
|||||
||||| 392 TGACAAAGAGTGGCTTCTGCTGAAGCGCAACCTGGACACCTACAGAGCGACTGG 451
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||||| 421 TTTCTACTGGCG 432
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||||| 452 TTTCTACTGGCG 463
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RESULT 6
CB481980
LOCUS
DEFINITION
  jns85.C09.f jns Sus scrofa cDNA 5', mRNA sequence.
ACCESSION
  CB481980
VERSION
  CB481980.1 GI:29288366
KEYWORDS
  EST.
SOURCE
  Sus scrofa (pig)
ORGANISM
  Sus scrofa
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
  1 (bases 1 to 461)
REFERENCE
  Neilan,J.G., Kutish,G.F., Lu,Z., Zsak,A. and Rock,D.L.
  Sequence analysis of African swine fever virus infected and
  non-infected porcine macrophage cDNA libraries
  Unpublished (2003)
  Contact: Neilan JG
  Plum Island Animal Disease Center
  US Department of Agriculture, Agricultural Research Service
  PO Box 848, Greenport, NY 11944-848, USA
  Tel: 631 323 3133
  Fax: 631 323 3044
  Email: jneilan@piadc.ars.usda.gov
  Single pass sequencing. Bases called with phred v0.020425.c and
  trimmed with the aid of the trim alt option. Vector identified by
  cross match v0.90329 and Lucy v1.17p.
  Seq primer: M13 forward.
  Location/Qualifiers
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    /db_xref="taxon:9823"
    /tissue_type="lymphoid"
    /cell_type="macrophage"
    /lab_host="DH10B"
    /clone_lib="jns"
    /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI;
    Library made from pools of polyA selected RNA. Macrophages
    were derived from peripheral blood mononuclear cells
    cultured for 48 hrs on plastic in the presence of 30% L929
    supernatant."
  ORIGIN
    source
    54.6%; Score 323; DB 14; Length 461;
    Query Match 84.8%; Pred. No. 1.2e-68;
    Best Local Similarity

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Matches 362; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 2 CTGCTCCACTGCTCTGTGGGATCATGGAATTCGACTGCTGTGGGCTGGTGGTG 61
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QY 62 ATGGCTGGTGTATTCGAATCCAGGCGGGATCCTGAACTGGAACAGATGGTCAAGCAA 120
Db 367 TTGTGCTGGTGTATTCGAATCCAGGCGGGATCCTGAACTGGAACAGATGGTCAAGCAA 161
QY 122 GTGACTGGGAAATGCCATCCTCTACTGACGAGGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 307 GTGACCGGGAAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 221
QY 182 GGCAGAGGCCCAACCCAAAGATGCCAGGACTGGTGTGCTGCGACCCCATGACTGCTAT 248
Db 247 GGCAGAGGTGAACCCAAAGATGCCAGACTGGTGTGCTGCGACCCCATGACTGCTAT 296
QY 242 GACCACTGAAGACCCAGGGGTGGGATCTCAAGGACTTATTACAGATCAACACTTTTCC 301
Db 187 AGTCACCTGAAGGCGCATGGCTCGGCACCCACTTGGACCACTACAGATACACTTTTCC 341
QY 302 CAGGGAACATCAGCTGCTGTGCAAGGGAAGTGTGTGAGCAGCAGCTGTGTGCTGTG 355
Db 127 CAGGGACCGTCCAGTGTCTGTGCAAGGGGAGTGTGTGAGGCGAGAGCTGTGCGCTGT 401
QY 362 GACAAGAGGTGGCTTTCTGCTTGAAGCGCAAGCTGGACACTTACAGAGGAGCTGCGT 421
Db 67 GACAAGGGGTGGCTTTCTGCTGATGAAGCGGAACCTGGACAGCTACAGAGGACCTGCGT 8
QY 422 TTCTACT 428
Db 7 TACTACT 1

RESULT 7
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LOCUS
DEFINITION
EST4080 human nasopharynx Homo sapiens cDNA, mRNA linear EST 25-JUN-2003
ACCESSION
CD687559
VERSION
CD687559.1 GI:32205515
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
CONTACT: Vixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsums.edu.cn.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
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/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 52.1%; Score 308.6; DB 14; Length 424;
Best Local Similarity 96.3%; Pred. No. 3.9e-65;
Matches 369; Conservative 0; Mismatches 9; Indels 5; Gaps 5;
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Db 42 TCTGCTCCACTGCTCTGTGCTGGATCATGGAATTCGACTGCTGTGGGCTGGTGGT 101
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Db 102 GATGGCTGGTGTGATTCGAATCCAGGCGGGATTCCTGAACTGGAACAGATGGTCAAGCAA 161
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Db 162 AGTACTGGGAAATGCCATCCTCTCTACTGCGCTACGGCTGTGCTGCGGACTAGG 221
QY 181 TGGCAGAGGCC-AAACCAAGATGCCAGGACTGGTGTGCTGCGGACCCATGACTGCTGCT 239
Db 222 TGGGAGAGGCCGAAGCAAGATGCCAGGACTGGTGTGCTGCGGACCCATGACTGCTGCT 281
QY 240 ATGACCACCTGGAAGACCCAGGGGTGGG-CATCTACAAGGA-CTATTACAGATA-CAACT 296
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QY 356 GCCTGTGACAAGGAGTGGCCTT 378
Db 402 GCCTGTGACAAGGAGTGGCCTT 424

RESULT 8
BY752231
LOCUS
DEFINITION
BY752231 RIKEN full-length enriched, activated spleen Mus musculus
cDNA clone F830213F07 5', mRNA sequence.
ACCESSION
BY752231
VERSION
BY752231.1 GI:27183012
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 623)
AUTHORS
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gibsi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Vexardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL
MEDLINE
22354683
```

12466851
 PUBLISHED
 COMMENT
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 The Institute of Physical and Chemical Research (RIKEN)
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 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in RIKEN.
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 Location/Qualifiers
 1. .623
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 /strain="NOD"
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 /clone="F830213F07"
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 Best Local Similarity 77.5%; Pred. No. 4.3e-62;
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 QY 2 CTGGCTCCACTGCTGTGCTGGGATCATGGAACTTGCATGCTGTGTGGCTGGTGGT 61
 Db 10 CTGGCTGCCTTGTCTGGCTGGAACTATGAGACTCGCCCTGCTGTGTGGCTGTGC-- 67
 QY 62 ATGGCTGGTGTGATTCATCCATCCAGGCGGGATCCTGAACCTGAAACAGATGGTCAAGCAA 121
 Db 68 -TGGCCGGTATAACTGCAACCCAGGAGGGCTCCTGAACTGAACCAAGATGGTCAACAC 126
 QY 122 GTGACTGGGAATGCCATCCTCTCTACTGCGCCCTACGGCTGCTACTCGGACTAGGT 181
 Db 127 ATGACGGGGAAGAAAGCCTTCTTCAGCTACTGCGCCCTACGGCTGTCTACTGTGACTGGT 186
 QY 182 GGCAGAGGCCCAACCCAAAGATGCGAGGACTGGTGTGCTGCCAGACCCCATGACTGCTGCTAT 241
 Db 187 GGCAGAGGCCCAACCCAAAGATGCGAGGACTGGTGTGCTGTGCTGCTGCTGCTGCTGCTAT 246
 QY 242 GACCACCTGAGACCCAGGGGTGGGATCTTACAGGACTATTACAGATACAACTTTTCC 301
 Db 242 GACCACCTGAGACCCAGGGGTGGGATCTTACAGGACTATTACAGATACAACTTTTCC 301

247 GCCCACCCTGAAGATCGATGATGATGCAAGAGCCTGACACAACTACAATACAGCATCTCC 306
 QY 302 CAGGGGAACATCCACTGCTCTGTACAAAGGAAGCTGGTGTGAGCAGCAGCTGTGTGCTGT 361
 Db 307 CAGGGCACTATCCAGTGTCTGTGCAACAGGGAGCTGGTGTGAAGGCACTGTGTGCTGT 366
 QY 362 GACAAGAGGTGGCTTCTGCTCAAGGCAACCTGGACACCTACCAAGAGCACTGGT 421
 Db 367 GACAAGAGGTGGCTTGTGCTTGAAGCANAACTGGATAGCTACAATAAGGCGCTGTGCT 426
 QY 422 TTCTACTGGCGGCCCACTGCGCGGGGAGACCCCTGGTGTGCTAGAGCCACACCTCT 481
 Db 427 TACTACTGGCGGCCCTGGTGTGCAAGGCAAGACTCCAGCATGCTAAGGGAGTCCACTCTGT 486

RESULT 9
 LOCUS AK018005
 DEFINITION Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830452G11 product:phospholipase A2, group IID, full insert sequence.
 ACCESSION AK018005
 VERSION AK018005.1 GI:12857529
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 1582)
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirakawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,

Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Taya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAAGTCAAGCAAGCTCTTTTCTTTTCTTWN 3'], cDNA was prepared by using triphosphate thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAATCTCGATTAATTAATATATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from lambda FUC I. Cloning sites, 5' end SalI; 3' end: BamHI. Host: DH10B

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QY	2	CTGCGTCCACTGCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGCGCTGTGTGGTG	61	
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QY	62	ATGGCTGTGTGATTCCAATCAGGGCGGGATCCTGAACCTGAAACAAGATGTTCAAGCAA	121	
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QY	122	GTGACTGGGAAAATGCCCATCTCTCTACTGCGCCCTACGGCTGTCACTGCGGACTAGGT	181	
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ORIGIN

Query Match 45.4%; Score 268.8; DB 9; Length 501;
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Matches 324; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

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QY 365 AAGGAGTGGCTTCTGCTTGAAGCGCAACCTGGACACTACAGAGGAGCTGCGTTTC 424
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Db 361 TACTGGCGGCGCGCTGTGCAAGGCAAGACTCCAGCATGCTAAGGAGTCCACTCTGT 417

RESULT 13

BQ418599

LOCUS

DEFINITION BQ418599 601 bp mRNA linear EST 23-MAY-2002
ik55a07.y1 Kaestner ngn3 wt Mus musculus cDNA 5' similar to
TR:Q9WVF6 Q9WVF6 GROUP IID SECRETED PHOSPHOLIPASE A2 ;, mRNA
sequence.

ACCESSION

BQ418599

VERSION

BQ418599.1

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 601)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemiska, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,

Schmitt, A., Theising, B., Ritter, F., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,

TITLE
JOURNAL
COMMENT

Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ik55a07.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bioh.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Marie Scearce
(mscearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 456.

FEATURES
source

Location/Qualifiers
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Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The cDNA's were prepared with an oligo containing a
NotI site, and SalI linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-SalI sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/- . The wt library is in
pSPORT1, T7 promoter is 5'."

ORIGIN

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Best Local Similarity 77.7%; Pred. No. 1.6e-54;
Matches 321; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 69 GTGTGATTCCTCAATCCAGGGCGGGATCTCTGAACCTCAACAGATGCTCAAGCAAGTGACTG 128
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Db 468 GCGGGCCCCGTTGCAAGGCAAGCAACTCCAGCATGCTTAAGGGAGTCCACTCTGT 520

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cdna library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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ORIGIN
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Best Local Similarity 79.3%; Pred. No. 2.1e-54;
Matches 315; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
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VERSION AK004232.1
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci P. and Hayashizaki Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2

Contact: Yoshihide Hayashizaki
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome.res@gsc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

```

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED 11042159

REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagao, K., Sasaki, N., Carninci, P., Komano, H., Akiyama, J., Nishi, K., Kitesunai, T., Tashiro, H., Itoh, M., Sumi, Y., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, F., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED 11076861

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6

JOURNAL

REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirakawa, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komano, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Teijima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCGCACTCGACTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGATCCAGAGCTCAATTAATTAATTAACCCCGCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES

source

Location/Qualifiers

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ORIGIN

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Best Local Similarity 79.3%; Pred. No. 2.3e-54;
Matches 315; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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8	284.2	48.0	496	6	AX464400	AX464400 Sequence
9	284.2	48.0	496	6	AX697309	AX697309 Sequence
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27	110.8	18.7	854	6	I09230	I09230 Sequence 34
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29	110.8	18.7	854	6	AX337559	AX337559 Sequence
30	110.8	18.7	854	6	AX587679	AX587679 Sequence
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34	110.8	18.7	1116	6	BD194533	BD194533 Human nuc
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38	109.8	18.5	222086	2	AC106106	AC106106 Rattus no
39	109.8	18.5	239739	2	AC116054	AC116054 Rattus no
40	109.8	18.5	282515	2	AC118094	AC118094 Rattus no
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44	104.8	17.7	1445	10	MMU18119	U18119 Mus musculu
45	104.8	17.7	1480	10	BC029347	BC029347 Mus muscu

ALIGNMENTS

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LOCUS AF112982 878 bp mRNA linear PRI 30-AUG-1999
DEFINITION Homo sapiens group IID secretory phospholipase A2 (PLA2) mRNA,
complete cds.
ACCESSION AF112982
VERSION AF112982.1 GI:5771419
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS Ishizaki,J., Suzuki,N., Higashino,K., Yokota,Y., Ono,T.,
Kawamoto,K., Fujii,N., Arita,H. and Hanasaki,K.

TITLE Cloning and characterization of novel mouse and human secretory phospholipase A2(s)
J. Biol. Chem. 274 (35), 24973-24979 (1999)
MEDLINE 99386983
PUBMED 10451175
REFERENCE 2 (bases 1 to 878)
Ishizaki, J., Suzuki, N., Higashino, K. and Hanaeaki, K.
Direct Submission
Submitted (11-DEC-1998) Shionogi Research Laboratories,
Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002, Japan
JOURNAL Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.3e-139;
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTGCCTCCACGCTGCTGTGGGATCATGAACTTGCACTGCTGTGTGGCTGGTGT 60
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DB 481 TACCTGTCTCAGCATGAGCTCTGGCATCCCCCTCCACCTCAGTATCTAACTGAACCCAGC 540

QY 541 CTGGCTTTTCAACACTCCGGGGGAGGTAGTCCAGCTCCCGGAACCC 592
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LOCUS Homo sapiens phospholipase A2 (SPLASH) mRNA, complete cds.
DEFINITION
ACCESSION AF188625
VERSION AF188625.1 GI:6453792
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1938)
AUTHORS Shakhov, A.N., Rubtsov, A.V., Lyakhov, I.G., Tumanov, A.V. and Nedospasov, S.A.
TITLE SPLASH (PLA2IID), a novel member of phospholipase A2 family, is associated with lymphotoxin deficiency
JOURNAL Genes Immun. 1 (3), 191-199 (2000)
MEDLINE 21040292
PUBMED 11196711
REFERENCE 2 (bases 1 to 1938)
AUTHORS Shakhov, A.N., Rubtsov, A.V., Lyakhov, I.G., Tumanov, A.V. and Nedospasov, S.A.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-1999) Laboratory of Molecular Immunoregulation,
IRSP, SAIC, NCI-FCRDC, P.O. Box B, Frederick, MD 21702, USA
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CDS
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ORIGIN
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Best Local Similarity 99.8%; Pred. No. 5.7e-139;
Matches 591; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTGCCTCCACGCTGCTGTGGGATCATGAACTTGCACTGCTGTGTGGCTGGTGT 60
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QY 61 GATGGCTGTGTGATTCCTCAATCCAGGGCGGATCTCTGAACCTGAAACAGATGGTCAAGCA 120
DB 69 GATGGCTGTGTGATTCCTCAATCCAGGGCGGATCTCTGAACCTGAAACAGATGGTCAAGCA 128
QY 121 AGTACTGGGAAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCTACCTGGGACTAGG 180
DB 129 AGTACTGGGAAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCTACCTGGGACTAGG 188
QY 181 TGGCAGAGCCCAACCCAAAGATGCCAGCTGGTGTGCTGCCAGACCCATGCTGTGCTA 240
DB 189 TGGCAGAGCCCAACCCAAAGATGCCAGCTGGTGTGCTGCCAGACCCATGCTGTGCTA 248
QY 241 TGACCACTTGAGACCCAGGGTGGCGCATCTACAAGGACTATTACAGATACACTTTTC 300

Db 249 TGACCACCTGAAGACCCAGGGGTGACGACTTACAGGACTATTACAGATACAACTTTTC 308

QY 301 CCAGGGGAACATCCACTGCTCTGACAGGGAAGCTGTGTGAGCAGCAGCTGTGTGCTG 360

Db 309 CCAGGGGAACATCCACTGCTCTGACAGGGAAGCTGTGTGAGCAGCAGCTGTGTGCTG 368

QY 361 TGACAGGAGGTGGCTTCTGCTGAGCGCAACCTGGACACCTTACAGAGCGAGCTGCG 420

Db 369 TGACAGGAGGTGGCTTCTGCTGAGCGCAACCTGGACACCTTACAGAGCGAGCTGCG 428

QY 421 TTCTACTGCGGCCCGCCACTGCGGGGGGAGACCCCTGGGTGTAGAGCCACACCTC 480

Db 429 TTCTACTGCGGCCCGCCACTGCGGGGGGAGACCCCTGGGTGTAGAGCCACACCTC 488

QY 481 TACCCTGTTCTCAGCATGAGCTCTGGCATCCCACTCCCACTCAGTATCTAACTGAACAGC 540

Db 489 TACCCTGTTCTCAGCATGAGCTCTGGCATCCCACTCCCACTCAGTATCTAACTGAACAGC 548

QY 541 CTGGCTTTTCAACACTCGGGGGGAGGTAGTCCAGCCCTCCCGGAACCC 592

Db 549 CTGGCTTTTCAACACTCGGGGGGAGGTAGTCCAGCCCTCCCGGAACCC 600

RESULT 3

BC025706

LOCUS

DEFINITION

Homo sapiens phospholipase A2, group IID, mRNA (cdna clone

MG:34386 IMAGE:5223912), complete cds.

ACCESSION

BC025706

VERSION

BC025706.1 GI:19344000

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 2747)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altshuler,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusik,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Schettz,J.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abrahamson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Rulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Sanchez,A., Whiting,M., Madan,A., Madan,A., Rodriguez,S.,

Bouffard,G.G., Blakesley,R.W., Young,A.C., Shevchenko,Y.,

Dickson,M.C., Rodriguez,A.C., Touchman,J.W., Green,E.D.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Schmutz,J., Myers,R.M.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2747)

Strausberg,R.

Direct Submission

Submitted (06-MAR-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help Desk

Email: cgabs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 49 Row: m Column: 9

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 21314652.

FEATURES

Location/Qualifiers

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/note="Vector: pCMV-SPORT6"

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78..386

/note="Phoslip; Region: Phospholipase A2. Phospholipase A2

releases fatty acids from the second carbon group of

glycerol. Perhaps the best known members are secreted

snake venoms, but also found in secreted pancreatic and

membrane-associated forms. Structure is all-alpha, with

two core disulfide-linked helices and a calcium-binding

loop. This alignment represents the major family of PLA2s.

A second minor family, defined by the honeybee venom PLA2

PDB:1POC and related sequences from Gila monsters

(Heloderma), is not recognized. This minor family

conserves the core helix pair but is substantially

different elsewhere"

/db_xref="CDD:pfam00068"

ORIGIN

Query Match 97.9%; Score 579.4; DB 9; Length 2747;

Best Local Similarity 99.8%; Pred. No. 3.5e-136;

Matches 580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGCTCTGTGCTGGGATCATGGAATTGCACTGCTGTGTGGGCTGGTGTGCTGTG 71

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QY 72 TGATTCCAATCCAGGGGGGAGTCTTGACCTGGAACAGATGGTCAAGCAAGTCACTGGA 131

Db 61 TGATTCCAATCCAGGGGGGAGTCTTGACCTGGAACAGATGGTCAAGCAAGTCACTGGA 120

QY 132 AAATGCCCATCTCTCTCTACTGGCCCTACGCTCTGCTCGGACTAGGTGGCAGAGGCC 191

Db 121 AAATGCCCATCTCTCTCTACTGGCCCTACGCTCTGCTCGGACTAGGTGGCAGAGGCC 180

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DEFINITION Homo sapiens clone DNA76538 PLA2G2D (UNQ768) mRNA, complete cds.
ACCESSION AY358606
VERSION AY358606.1 GI:37182333
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 496)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heidens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Stinson,J., Seshagiri,S., Simmons,I., Singh,J., Smith,V.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Watanabe,C., Wiedand,D., Woods,K.,
Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 496)
AUTHORS Clark,H.F.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
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location/Qualifiers
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/db_xref="taxon:9606"
/clone="DNA76538"
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ORIGIN

Query Match 48.0%; Score 284.2; DB 9; Length 496;

Best Local Similarity 97.3%; Pred. No. 2.7e-61;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Db 241 TGACCACTTGAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACCTT 297

RESULT 11
LOCUS AF124374 904 bp mRNA linear ROD 06-JUL-1999
DEFINITION Mus musculus group IID secreted phospholipase A2 (Pla2a2) mRNA,
complete cds.
ACCESSION AF124374
VERSION AF124374.1 GI:5359707
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 904)
AUTHORS Valentini,E., Koduri,R.S., Scimeca,J.C., Carle,G., Gelb,M.H.,
Lazdunski,M. and Lambeau,G.
TITLE Cloning and recombinant expression of a novel mouse-secreted
phospholipase A2
JOURNAL J. Biol. Chem. 274 (27), 19152-19160 (1999)
PUBMED 99315857
REFERENCE 2 (bases 1 to 904)
AUTHORS Valentini,E., Koduri,R.S., Scimeca,J.C., Carle,G., Gelb,M.H.,
Lazdunski,M. and Lambeau,G.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1999) CNRS, IPMC, Sophia Antipolis, 660 route des
Lucioles, Valbonne 06560, France
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Best Local Similarity 77.3%; Pred. No. 6e-61;


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/db_xref="GI:10862734"
/db_xref="SPTREMBL:Q9H507"
/translation="MSMPLIQPEGTHSLRPSPTQQSQSDSGHRTW"
17434. .17473 /note="AluSx repeat: matches 1. .309 of consensus"
repeat_region 17754. .17885 /note="FLAM C repeat: matches 1. .132 of consensus"
misc_feature complement(17768. .18077)
/note="match: GSS: Em:AQ880240"
17957. .18057 /note="MERSA repeat: matches 10. .109 of consensus"
repeat_region 18254. .18995 /note="L1M2 repeat: matches 5582. .6328 of consensus"
repeat_region 19004. .19128 /note="FAM repeat: matches 1. .124 of consensus"
repeat_region 19139. .19511 /note="L1M2 repeat: matches 5204. .5592 of consensus"
repeat_region 19567. .19724 /note="MER63 repeat: matches 1. .783 of consensus"
repeat_region 19867. .20140 /note="AluJo repeat: matches 1. .265 of consensus"
repeat_region 20141. .20440 /note="AluJb repeat: matches 2. .297 of consensus"
repeat_region 20441. .20476 /note="AluJo repeat: matches 265. .301 of consensus"
repeat_region 20531. .20547 /note="L1M4 repeat: matches 4735. .4751 of consensus"
repeat_region 20548. .20844

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/note="AluSx repeat: matches 1. .297 of consensus"
20845. .20978 /note="L1M4 repeat: matches 4751. .4891 of consensus"
20979. .21283 /note="AluSx repeat: matches 1. .306 of consensus"
21284. .21593 /note="L1M4 repeat: matches 4891. .5163 of consensus"
21594. .21892 /note="AluSp repeat: matches 1. .301 of consensus"
21893. .21968 /note="L1M4 repeat: matches 5163. .5242 of consensus"
22116. .22295 /note="L1M4 repeat: matches 5319. .5503 of consensus"
misc_feature complement(22408. .23261)
/note="match: GSS: Em:AQ743836"
22535. .22832 /note="AluJb repeat: matches 3. .312 of consensus"
22849. .23054

Query Match 45.9%; Score 272; DB 9; Length 98743;
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CTGACAAAGGAGCTGCTGTGAGCAGCAGCTGTGCTGTGACAGGAGGTGGCCTTCT 380
Db 67401 CTGACAAAGGAGCTGCTGTGAGCAGCAGCTGTGCTGTGACAGGAGGTGGCCTTCT 67342
QY 381 GCGTGAAGCGCAACCTGGACACCTACCAAGAGCAGCTGGTTCCTACTGGCGGCCCACT 440
Db 67341 GCGTGAAGCGCAACCTGGACACCTACCAAGAGCAGCTGGTTCCTACTGGCGGCCCACT 440
QY 441 GCGGGGGGAGAGCCCTGGTGTGTAGAGCCACACCTCTACCTGTTCCTCAGCATGG 500
Db 67281 GCGGGGGGAGAGCCCTGGTGTGTAGAGCCACACCTCTACCTGTTCCTCAGCATGG 67222
QY 501 AGCTCTGGCATCCCACTCAGTATCTACCTGAAGCCACCTCTACCTGTTCCTCAGCATGG 560
Db 67221 AGCTCTGGCATCCCACTCAGTATCTACCTGAAGCCACCTCTACCTGTTCCTCAGCATGG 67162
QY 561 GGGGGAGGTAGTCCAGCCTCCCGGGAACCC 592
Db 67161 GGGGGAGGTAGTCCAGCCTCCCGGGAACCC 67130

RESULT 13
E37202 LOCUS
E37202 DEFINITION
E37202 Mouse secretory phospholipase A2.
E37202 ACCESSION
E37202.1 GI:18626612 VERSION
E37202.1 JP 2000166544-A/1. KEYWORDS
Mus musculus (house mouse) SOURCE
Mus musculus ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 501)
AUTHORS Ishizaki,J., Suzuki,N. and Hanasaki,K.
TITLE Mouse secretory phospholipase A2
JOURNAL Patent: JP 2000166544-A 1 20-JUN-2000;
SHIONOGI & CO LTD
COMMENT OS Mus musculus (mouse)
PN JP 2000166544-A/1
PD 20-JUN-2000
PF 09-DEC-1998 JP 1998349602
PR
PI JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI
PC C12N9/16, C12N5/10, C12N15/09, C12Q1/44, G01N33/15// (C12N9/16, PC
C12R1:91),
PC (C12N5/10, C12R1:91), (C12N15/09, C12R1:91), C12N5/00, C12N15/00,
PC (C12N5/00, C12R1:91), (C12N15/00, C12R1:91)
CC
FH Key Location/Qualifiers
FT source 1. .501

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FEATURES
source
FT Location/Qualifiers
1..501
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
ORIGIN
Query Match 45.4%; Score 268.8; DB 6; Length 501;
Best Local Similarity 77.7%; Pred. No. 2.2e-57;
Matches 324; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
Qy 65 GCTGGTGTATCAATCCAGGGGGATCTGTAACCTGCAAGAGATGGTCAAGATG 124
Db 1 GCGGNTATTAATCTGCAACCCAGGGGGCTCTGTAACCTGCAAGAGATGGTCAACATG 60
Qy 125 ACTGGGAAATGCCCATCTCTCTTACTGCGCCCTAGCGCTCTCACTGCGGACTAGTGGC 184
Db 61 ACGGGGAAGAAGCCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 185 AGAGGCCAACCAAGATGCCAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
Db 121 AAAGGGCAACCAAGATGCCAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy 245 CACCTGAAGACCCAGGGGTGGGCACTTACAGGACTTATACAGATACAACTTTTCCAG 304
Db 181 CACCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
Qy 305 GGGAAATCCATCTCTGCAAGGAAAGTGGTGTGAGCAGCAGCAGCAGCAGCAGCAGCAG 364
Db 241 GGCACATCCAGTCTGCAACGGAGCTGGTGTGAAGGCAACTGCTGCTGCTGCTGCTG 300
Qy 365 AAGAGGTGGCTTCTGCTGAGCGCAACCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 424
Db 301 AAGAGGTGGCTTCTGCTGAGCGCAACCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 360
Qy 425 TACTGCGCGCCCACTGCGGGGGAGACCCCTGGGTGTAGAAGCCCAACCCCTCT 481
Db 361 TACTGCGCGCCCGTGTGAAGGCAAGCTCCAGCATGCTAAGGGAGTCCACTCTGT 417

RESULT 14
CPIIPHA2
LOCUS
DEFINITION
C.porcine mRNA for typeII phospholipase A2.
ACCESSION
X82631
VERSION
X82631.1 GI:951010
KEYWORDS
phospholipase a2.
SOURCE
Cavia porcellus (domestic guinea pig)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
REFERENCE
1 Vial,D., Senorale-Pose,M., Havet,N., Molio,L., Vargaftig,B.B. and Touqui,L.
Expression of the type-II phospholipase A2 in alveolar macrophages. Down-regulation by an inflammatory signal
J. Biol. Chem. 270 (29), 17327-17332 (1995)
MEDLINE
95340522
PUBMED
7615534
REFERENCE
2 (bases 1 to 760)
AUTHORS
Vial,D.
TITLE
Direct Submission
SUBMITTED (10-NOV-1994) D. Vial, Institut Pasteur, 25 rue du Dr. Roux, 75015 Paris, FRANCE
LOCATION/Qualifiers
1..760
/organism="Cavia porcellus"
/mol_type="mRNA"
/db_xref="taxon:10141"
/cell_type="alveolar macrophage"
/dev_stage="adult"
FEATURES
source

Query Match 22.6%; Score 133.8; DB 10; Length 760;
Best Local Similarity 55.5%; Pred. No. 3.7e-23;
Matches 258; Conservative 0; Mismatches 207; Indels 0; Gaps 0;
Qy 26 ATCATGAACCTTGCACTGCTGTGGGCTGTGGTGTGATGGTGTGATTCCTCAATCCAG 85
Db 51 AGCATGAAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 110
Qy 86 GCGGGATCTCGAATCAACCAAGATGCTCAAGCAAGTGAAGTGGGAAATGCCCATCTCTC 145
Db 111 GGACACTTGAAGCAATTCACAGAAATGATCAAGCTCACAGAGGAAAGATGGACTTACA 170
Qy 146 TCCTACTGGCCCTAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205
Db 171 AGTTATGGCCCTAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 230
Qy 206 ACGGACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
Db 231 ACAGATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 290
Qy 266 GGCATCTACAGGACTTATACAGATACAACTTTCCAGGGGNAACATCCACTGCTCTGAC 325
Db 291 GGCACGAAATTTCTGAACCTTACCGCTTACCCATAAGGGAGCTCGATCACTGCTGTA 350
Qy 326 AAGGGAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 385
Db 351 AAGCAGAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 410
Qy 386 AAGCGCAACTCTGCAACCTTACCAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445
Db 411 GCTGCAAACTGAAAGTTATAGCAGAAGTACCACTTTTATACAAATGGACTGTGCGGC 470
Qy 446 GGCAGACCCCTGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
Db 471 GGAAGACCCCGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 515

RESULT 15
AR274880
LOCUS
DEFINITION
Sequence 17 from patent US 6506607.
ACCESSION
AR274880
VERSION
AR274880.1 GI:29707430
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 1016)
AUTHORS
Shyjan,A.W.
TITLE
Methods and compositions for the identification and assessment of prostate cancer therapies and the diagnosis of prostate cancer
JOURNAL
Patent: US 6506607-A 17 14-JAN-2003;
FEATURES
Location/Qualifiers
1..1016
/organism="unknown"
source


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ORIGIN /mol_type="genomic DNA"
Query Match 20.2%; Score 119.6; DB 6; Length 1016;
Best Local Similarity 58.0%; Pred. No. 1.5e-19;
Matches 231; Conservative 0; Mismatches 164; Indels 3; Gaps 1;

QY 67 TGGTGTGATTCCAAATCCAGGCGGGATCTTGAACCTGAACAAGATGGTCAAGCAAGTGAC 126
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
171 TAGTGTGCCTGCTGTGCAAGGAGGCTTGTGGACCTAAATCAATGATCGAAGGTGAC 230
QY 127 TGGGAAATGCCCATCTCTCTACTTGGCCCTAGGCGTGTCACTGCGGACTAGGTGGCAG 186
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
231 AGGGAAGAACGCCCTGACAAACTACGGCTTCTACGGCTGTACTGCGGCTGGGGCGGCCG 290
QY 187 AGGCCAACCCAAAGATGCCACGACTGGTGTCTGCCAGACCCATGACTGTGCTATGACCA 246
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
291 AGGAACCCCAAGGATGGCACCGATTGGTGTCTTGGGCGCATGACCACTGTCTATGGCG 350
QY 247 CCTGAAGACCCAGGGGTGGGATCTACAAGGACTATTACAGATAACAACCTTTCCCAAGG 306
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
351 GCTGGAGGAGAGGGGTGCAACATTGGCACACAGTCTCTACAAATACAGATTCGCGTGGG 410
QY 307 GAACATCCACTGCTCTGACAAGGAGAGCTGGTGTGACAGCAGCTGTGTGCTGTGACAA 366
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
411 CGTGTACCTGC---GAGCCCGGGCCCTTCTGCCATGTGAACCTCTGTGCCTGTGACCG 467
QY 367 GGAGGTGGCTTCTGCTGAAGCGCAACCTGGACACCTACCAAGACGACTGGTTTCTA 426
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
468 GAAGCTCGTCTACTGCTCAAGAGAAACCTACGGAGCTAACACCCACAGTACCAATACTT 527
QY 427 CTGGGGGGCCCACTGCGGGGGGACAGCCCTGGGTGCT 464
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
528 TCCCAACATCCTCTGCTCTAGGCCCTCCCGCAGCGAGCT 565

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Job time : 2407.28 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2004, 11:14:15 ; Search time 251.748 Seconds
(without alignments)
9989.875 Million cell updates/sec

Title: US-09-830-321A-4
Perfect score: 592
Sequence: 1 tctgctccactgctctgtg.....ccagctcccccggaacc 592

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	100.0	592	3	AAA53269 Human pho
2	592	100.0	878	3	AAA60878 Human sec
3	579.4	97.9	2747	7	ACC72857 Human can
4	575.4	97.2	854	4	AA514884 Human can
5	568.8	96.1	1927	4	AAH98759 Human EST
6	568.8	96.1	1927	4	AAH99768 Human pro
7	567.4	95.8	1931	5	AAAD19218 Human CG9
8	296	50.0	1233	3	AAA60866 Mouse sec
9	296	50.0	1233	3	AAA72076 cDNA enco
10	284.2	48.0	496	3	AAA77684 Human PRO
11	284.2	48.0	496	4	AAF54466 DNA enco
12	284.2	48.0	496	4	AA521510 Human cDN
13	284.2	48.0	496	7	ACD24119 Novel hum
14	284.2	48.0	496	7	ACA67260 cDNA enco
15	284.2	48.0	496	7	ACA03869 cDNA enco
16	284.2	48.0	496	7	ABX89407 DNA enco
17	284.2	48.0	496	7	ACD42061 Human sec
18	284.2	48.0	496	8	ACA04290 Human cDN
19	284.2	48.0	496	8	ADA46052 Novel hum
20	284.2	48.0	496	8	ADA76483 Human PRO
21	284.2	48.0	496	8	ADA19133 Human PRO
22	284.2	48.0	496	8	ADA61756 Homo sapi
23	284.2	48.0	496	8	ADB19541 Novel hum

ALIGNMENTS

RESULT 1
AAA53269
ID AAA53269 standard; cDNA; 592 BP.
XX
AC AAA53269;
XX
DT 05-OCT-2000 (first entry)
XX
DE Human phospholipase 1 HPPL1 coding sequence.
XX
KW Human; phospholipase 1; HPPL1; cancer; autoimmune disorder;
KW inflammatory disorder; reproductive disorder; infection; ss.
XX
OS Homo sapiens.

Location/Qualifiers
29..466

/tag= a
/product= "HPPL1"

29..91
/tag= b

/note= "this is a putative signal peptide"
29..76
/tag= c

/note= "this is a putative signal peptide"
77..463
/tag= d

/note= "this is a putative mature HPPL1"
92..463
/tag= e

/note= "this is a putative mature HPPL1"
WO200024911-A2.

04-MAY-2000.

27-OCT-1999; 99WO-US025021.

27-OCT-1998; 98US-00181317.

21-JAN-1999; 99US-00234726.

(INCY-) INCYTE PHARM INC.

Hillman JL, Bandman O, Guegler KJ, Corley NC, Baughn MR;

Azimzai Y, Lal P, Lu DAM;

PN	WO200154477-A2.	
XX	02-AUG-2001.	
PD	25-JAN-2001; 2001WO-US002687.	
XX	25-JAN-2000; 2000US-00491404.	
XX	17-JUL-2000; 2000US-00617746.	
PR	03-AUG-2000; 2000US-00631451.	
PR	15-SEP-2000; 2000US-00663870.	
XX	(HYSE-) HYSEQ INC.	
PA	Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;	
XX	Cao Y, Drmanac RA, Zhang J, Werhman T;	
PI	WPI; 2001-476164/51.	
XX	P-PSDB; AAM24100.	
DR	Isolated polypeptide for treatment of diseases, diagnostics, raising	
XX	antibodies and research use.	
PT	Claim 1; Page 599-600; 1275pp; English.	
XX	The present invention provides the protein and coding sequences of novel	
CC	proteins from a variety of organisms, including human, dog, cat, horse,	
CC	cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea	
CC	urchin and tomato. These were derived from expressed sequence tags (ESTs)	
CC	from the organism of interest. They can be used in diagnostic,	
CC	forensics, gene mapping, identification of mutations, to assess	
CC	biodiversity and for nutritional purposes. The present sequence is a cDNA	
CC	of the invention	
XX	Sequence 1927 BP; 413 A; 598 C; 480 G; 436 T; 0 U; 0 Other;	
SQ	Query Match	
	Best Local Similarity 96.1%; Score 568.8; DB 4; Length 1927;	
	Matches 573; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
QY	13 GCTGTGCTGGGATCATGGAACCTTGCACTGCTGTGTGGCTGGTGGTGGTGTGT 72	
DB	2 GCGGTGGAATTCGATCATGGAACCTTGCACTGCTGTGTGGCTGGTGGTGGTGT 61	
QY	73 GATTCATTCAGGGCGGGATCCTGAACCTGAACAGATGTCTCAAGCAAGTCACTGGGAA 132	
DB	62 GATTCATTCAGGGCGGGATCCTGAACCTGAACAGATGTCTCAAGCAAGTCACTGGGAA 121	
QY	133 AATGCCCATCTCTCTACTGCGCTTACGGCTGTCTACTCGGACTAGGTGGCAGAGCCA 192	
DB	122 AATGCCCATCTCTCTACTGCGCTTACGGCTGTCTACTCGGACTAGGTGGCAGAGCCA 181	
QY	193 ACCCAAGATGCCAGGACTGGTGTGCGCAGACCCATGACTGCTCTATGACCCCTGAA 252	
DB	182 ACCCAAGATGCCAGGACTGGTGTGCGCAGACCCATGACTGCTCTATGACCCCTGAA 241	
QY	253 GACCCAGGGTGGCGCATCTCAAGGACTATACAGATACAACTTTTCCAGGGGAAACAT 312	
DB	242 GACCCAGGGTGGCGCATCTCAAGGACTATACAGATACAACTTTTCCAGGGGAAACAT 301	
QY	313 CCATGCTCTCACAGGGAAGCTGGTGTGACGACGAGCTGTGCTGTGACAGGAGGT 372	
DB	302 CCATGCTCTCACAGGGAAGCTGGTGTGACGACGAGCTGTGCTGTGACAGGAGGT 361	
QY	373 GGCTTCTGCTGAAGGGCAACCTGGGATCTAGAGCCACACCTCTACCTGTTTCT 432	
DB	362 GGCTTCTGCTGAAGGGCAACCTGGGATCTAGAGCCACACCTCTACCTGTTTCT 421	
QY	433 GCGCCATGCGGGGGCAGACCTGGGATCTAGAGCCACACCTCTACCTGTTTCT 492	
DB	422 GCGCCATGCGGGGGCAGACCTGGGATCTAGAGCCACACCTCTACCTGTTTCT 481	
QY	493 CAGCATGAGCTCGGCATCCCACTCTAGTATCTAACCTGAACCAAGCTGGCTTTTCAA 552	

Db	482 CAGCATGGAGCTCTGGCATCCCACTCAGTATCTAACCTGAACCAAGCTGGCTTTTCAA 541
Qy	553 ACACCTCGGGGAGGTAGTCCAGGCTCCCGGGAACCC 592
Db	542 ACACCTCGGGGAGGTAGTCCAGGCTCCCGGGAACCC 581
RESULT 6	
AAH99768	
ID	AAH99768 standard; cDNA; 1927 BP.
XX	AC
XX	AAH99768;
XX	
DT	16-OCT-2001 (first entry)
XX	
DE	Human protein encoding cDNA sequence SEQ ID NO:603.
XX	
KW	Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW	antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW	antibacterial; endocrine; cardiant; cardiant; central nervous system; virucide;
KW	anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW	antiaggregant; haemostatic; vulnery; antidiabetic; osteopathic; eczema;
KW	dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW	neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW	immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW	antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW	cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW	genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW	thrombocytopaenia; diabetes; osteoporosis; severe combined immunodeficiency;
KW	allergic rhinitis; diabetes; multiple sclerosis; depression;
KW	Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW	neurological disorder; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200153455-A2.
XX	
PD	26-JUL-2001.
XX	
PF	22-DEC-2000; 2000WO-US035017.
XX	
PR	23-DEC-1999; 99US-00471275.
PR	21-JAN-2000; 2000US-00488725.
XX	25-APR-2000; 2000US-00552317.
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Drmanac RT;
XX	
DR	WPI; 2001-457603/49.
XX	P-PSDB; AAM25827.
PT	Isolated human polynucleotides encoding polypeptides, useful for the
XX	treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
PS	Claim 1; Page 636; 1217pp; English.
XX	
CC	AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC	AAM25963. The proteins can have activities based on the tissues and cells
CC	they are expressed in, such as: antiinflammatory; antirheumatic;
CC	antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC	central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC	cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;
CC	antidiabetic; cytostatic; neuroprotective; antiallergic; antiasthmatic;
CC	antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC	encoding them can be used in gene therapy, antisense therapy and vaccine
CC	production. The proteins and polynucleotides are useful for screening for
CC	agonists or antagonists of a protein and for the treatment and diagnosis of
CC	disorders associated with the activity of a protein e.g. inflammation,
CC	rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC	neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC	infections, autoimmunity, genetic diseases, haematopoietic disorders,

Db 133 TCTCTACTGGCCCTACGGTGTACACTGCGAGTACTAGTGGCAGAGGCCAACCCAAAGATG 192
QY 204 CCACGGACTGGTGTGTCGACAGACCATGACTGCTGTATGACCACTGAAGACCCAGGGGT 263
Db 193 CCACGGACTGGTGTGTCGACAGACCATGACTGCTGTATGACCACTGAAGACCCAGGGGT 252
QY 264 GCGCATCTACAGGACTATTACAGATACAACTTTTCCAGGGGAAACATCCACTGTCTTG 323
Db 253 GCGGCATCTACAGGACTATTACAGATACAACTTTTCCAGGGGAAACATCCACTGTCTTG 312
QY 324 ACAAGGAACTGGTGTGACAGCAGCTGTGTGCTGTGACAGAGAGTGGCTTTCGCC 383
Db 313 ACAAGGAACTGGTGTGACAGCAGCTGTGTGCTGTGACAGAGAGTGGCTTTCGCC 372
QY 384 TGAAGCGCACTGGACACCTACAGACGACTGCGTGTTCATGTCGCGGCCCACTGCC 443
Db 373 TGAAGCGCACTGGACACCTACAGACGACTGCGTGTTCATGTCGCGGCCCACTGCC 432
QY 444 GGGGCGAGCCCTGGTGTGCTAGAGCCACACCTTACCTGTTCCTCAGCATGGAGC 503
Db 433 GGGGCGAGCCCTGGTGTGCTAGAGCCACACCTTACCTGTTCCTCAGCATGGAGC 492
QY 504 TCTGGCATCCCCACCTCAGTATCTACCTGAACAGCCTGGCTTTTCAACACTCCGGGG 563
Db 493 TCTGGCATCCCCACCTCAGTATCTACCTGAACAGCCTGGCTTTTCAACACTCCGGGG 552
QY 564 GGAGGTAGTCCAGCCTCCCGCGGAACCC 592
Db 553 GGAGGTAGTCCAGCCTCCCGCGGAACCC 581

RESULT 8
AAA60866
ID AAA60866 standard; cDNA; 1233 BP.
AC AAA60866;
DT 02-NOV-2000 (first entry)
XX
XX
DE Mouse secretory phospholipase A2 nucleotide sequence SEQ ID NO:13.
KW Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory;
KW antibacterial; immunosuppressive; tranquiliser; antirheumatic;
KW antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis;
KW chronic rheumatoid arthritis; ss.
OS Mus musculus.

XX Key Location/Qualifiers
FH CDS 36..470
FT
FT
FT sig_peptide /product= "secretory phospholipase A2 (PLA2)"
FT 36..92
FT mat_peptide /tag= b
FT 93..467
FT /tag= c
XX
XX WO200034486-A1.
XX
XX 15-JUN-2000.
XX
XX 07-DEC-1999; 99WO-JP006844.
XX
XX 09-DEC-1998; 99JP-00349608.
XX (SHIO) SHIONOGI & CO LTD.
XX Ishizaki J, Suzuki N, Hanasaki K;
XX WPI; 2000-423429/36.
XX P-PSDB; AAB12536.
XX

PT Human secretory phospholipase A2 (PLA2) and its encoded gene for
PT diagnosis and treatment of secretory PLA2-associated diseases e.g. septic
PT shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid
PT arthritis.
XX Example 3; Page 35-36; 45pp; Japanese.
XX
CC The present invention describes human secretory phospholipase A2 (PLA2).
CC PLA2 has antiallergic, antiinflammatory, antibacterial, tranquiliser,
CC immunosuppressive, vulnerary, antirheumatic and antithrombotic activities.
CC Human secretory phospholipase A2 (PLA2), the gene encoding it and
CC antibodies against it are useful for the diagnosis and treatment of
CC secretory PLA2-associated diseases e.g. septic shock, trauma,
CC pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
CC present sequence encodes mouse PLA2, which is used in an example from the
XX present invention
SQ Sequence 1233 BP; 279 A; 337 C; 307 G; 310 T; 0 U; 0 Other;
Query Match 50.0%; Score 296; DB 3; Length 1233;
Best Local Similarity 77.5%; Pred. No. 1.7e-69;
Matches 372; Conservative 0; Mismatches 105; Indels 3; Gaps 1;
QY 2 CTGCTCCACTGCTCTGTCTGCGATCATGGAACCTGCACTGCTGTGGGTGGTGGT 61
Db 9 CTGCTCCCTTGTCTGTGGGTGGAACCTATGAGACTGCGCTGTGTGGGTGGTGGT 66
QY 62 ATGGCTGGTGTGATTCCAAATCCAGGCGGGGATCCCTGAACCTGAACAAGATGTCAGACAA 121
Db 67 -TGGCGGGTATAACTGCAACCCAGGAGGGCTCTGAACTGAACTGAACATGATGTCACAC 125
QY 122 GTGACTGGGAAAATGCCATCCTCTCTACTGGCCCTACGGCTGTCACTGCGGACTAGGT 181
Db 126 ATGACGGGGAGAAAGACCTTCTTCAGCTACTGCGCTACGGCTGTCACTGCGGACTTGGT 185
QY 182 GGCAGAGGCCAACCCAAAGATGCCAGGAGTGGTGTGCTGCGACACCCATGACTGTGCTAT 241
Db 186 GGCAGAGGCCAACCCAAAGATGCCAGGAGTGGTGTGCTGCGACACCATGATGTTGCTAT 245
QY 242 GACCACTGGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTCC 301
Db 246 GCGCACTGGAAGATCGATGATGCAAGAGCCCTGACAGACAACTACAATACAGATCTCC 305
QY 302 CAGGGAGACATCCACTGCTCTGCAAGGGAAGTGGTGTGAGCAGCAGCTGTGTCCTGT 361
Db 306 CAGGGCACTATCCAGTGTCTGTGACAAACGGGAGTGGTGTGAAAGGCAACTGTGTCTGT 365
QY 362 GACAGGAGTGGCTTCTGCTGAAGCGCAACCTGGAACCTACCAAGGAGTGGTGT 421
Db 366 GACAGGAGTGGCTTGTGCTTGAAGCAAAACCTGGATAGCTACATAAGGCGCTGGT 425
QY 422 TTCTACTGGGCGGCCCCACTGCGGGGGGAGACCCCTGGGTGCTAGAGCCCAACCCCTCT 481
Db 426 TACTACTGGGCGGCCCCGTTGCAAAAGGCAAGACTCCAGCATGCTAAGGAGTCCACTCTGT 485
RESULT 9
AAA72076
ID AAA72076 standard; cDNA; 1233 BP.
AC AAA72076;
XX
XX
XX 24-NOV-2000 (first entry)
XX cDNA encoding mouse secreted phospholipase A2.
XX Secreted phospholipase A2; PLA2; mouse; murine; recombinant production;
XX antibody; diagnosis; expressed sequence tag; EST; drug screening; ss.
XX Mus musculus.
OS
XX Key Location/Qualifiers
FH CDS 36..470
FT

CC	nucleotide and protein sequences used in the exemplification of the
CC	present invention
XX	
SQ	Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;
	Query Match 48.0%; Score 284.2; DB 3; Length 496;
	Best Local Similarity 97.3%; Pred. No. 1.9e-66;
	Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY	1 TCTGCTCCACCTGCTCTGTGCTGGGATCATGGAACCTTGCACTGCTGTGTGGGCTGGTGGT 60
DB	1 TCTGCTCCACCTGCTCTGTGCTGGGATCATGGAACCTTGCACTGCTGTGTGGGCTGGTGGT 60
QY	61 GATGGCTGTGTGATTCCTCAATCCAGGGGGGATCCTGAACCTGGAACAGATGGTCAAGCA 120
DB	61 GATGGCTGTGTGATTCCTCAATCCAGGGGGGATCCTGAACCTGGAACAGATGGTCAAGCA 120
QY	121 AGTGACTGGAAAATGCCCATCTCTCTACTTGGCCCTACGGCTGTCTCACTGCGGACTAGG 180
DB	121 AGTGACTGGAAAATGCCCATCTCTCTACTTGGCCCTACGGCTGTCTCACTGCGGACTAGG 180
QY	181 TGGCAGAGCCCAACCAAGATGCCACGACTGTGTGCTGCCAGACCATGACTGCTGCTA 240
DB	181 TGGCAGAGCCCAACCAAGATGCCACGACTGTGTGCTGCCAGACCATGACTGCTGCTA 240
QY	241 TGACCACCTGGAAGACCCAGGGGTGGCGCATCTACAAGSACTATTACAGATACAACTT 297
DB	241 TGACCACCTGGAAGACCCAGGGGTGGCGCATCTACAAGSACTATTACAGATACAACTT 297
RESULT 11	
AAF54466	
ID	AAF54466 standard; DNA; 496 BP.
XX	
AC	AAF54466;
DT	
XX	02-APR-2001 (first entry)
XX	DNA encoding protein of the invention #109.
DE	
XX	Secreted; transmembrane; gene therapy; ss.
KW	
XX	Unidentified.
OS	
XX	WO200078961-A1.
PN	
XX	28-DEC-2000.
PD	
XX	18-FEB-2000; 2000WO-US004342.
PF	
XX	23-JUN-1999; 99US-0141037P.
PR	20-JUL-1999; 99US-0144758P.
PR	26-JUL-1999; 99US-0145698P.
PR	01-SEP-1999; 99WO-US020111.
PR	29-OCT-1999; 99US-0162506P.
PR	30-NOV-1999; 99WO-US028313.
PR	02-DEC-1999; 99WO-US028551.
PR	16-DEC-1999; 99WO-US030095.
PR	05-JAN-2000; 2000WO-US000219.
PR	06-JAN-2000; 2000WO-US000376.
XX	
XX	(GETH) GENENTECH INC.
PA	
XX	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI	Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI	Pan J, Paoni NF, Roy WA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI	Williams PM, Wood WI;
XX	WPI; 2001-071395/08.
DR	
XX	
XX	Secreted and transmembrane proteins and nucleic acids designated PRO,
PT	useful as hybridization probes, in chromosome and gene mapping and gene
PT	therapy.

PR	06-JAN-2000;	2000WO-US000277.	Db	1	TTCTGCTCCACTGCTCTGCTGGGATCATGGAACCTTGACACTGCTGCTGGGCTGGTGGT	60
PR	06-JAN-2000;	2000WO-US000376.	QY	61	GATGGCTGGTGGTGAATCCAAATCCAGGGCGGGATCTTGAACCTGAAACAAGATGCTCAAGCA	120
PR	11-FEB-2000;	2000WO-US0003565.	Db	61	GATGGCTGGTGGTGAATCCAAATCCAGGGCGGGATCTTGAACCTGAAACAAGATGCTCAAGCA	120
PR	18-FEB-2000;	2000WO-US0004341.	QY	121	AGTGACTGGGAAAATGCCCATCTCTCTACTGSCCTACGGCTGTCTACGCGGACTAGG	180
PR	24-FEB-2000;	2000WO-US0004414.	Db	121	AGTGACTGGGAAAATGCCCATCTCTCTACTGSCCTACGGCTGTCTACGCGGACTAGG	180
PR	24-FEB-2000;	2000WO-US0004914.	QY	181	TGGCAGAGGCCAACCCCAAGATGCCAGGACTGGTGTGTCGACAGCCCATGACTGCTGCTA	240
PR	01-MAR-2000;	2000WO-US0005601.	Db	181	TGGCAGAGGCCAACCCCAAGATGCCAGGACTGGTGTGTCGACAGCCCATGACTGCTGCTA	240
PR	02-MAR-2000;	2000WO-US0005941.	QY	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	03-MAR-2000;	2000US-0187202P.	Db	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	10-MAR-2000;	2000WO-US0006319.	QY	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	15-MAR-2000;	2000WO-US0006884.	Db	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	20-MAR-2000;	2000WO-US0007377.	QY	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	21-MAR-2000;	2000WO-US0007532.	Db	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	30-MAR-2000;	2000WO-US0008439.	QY	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	17-MAY-2000;	2000WO-US013705.	Db	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	22-MAY-2000;	2000WO-US014042.	QY	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	30-MAY-2000;	2000WO-US014941.	Db	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	02-JUN-2000;	2000WO-US015264.	QY	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	05-JUN-2000;	2000US-0209832P.	Db	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	28-JUL-2000;	2000WO-US020710.	QY	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	11-AUG-2000;	2000WO-US022031.	Db	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	23-AUG-2000;	2000WO-US023522.	QY	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	24-AUG-2000;	2000WO-US023328.	Db	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	08-NOV-2000;	2000WO-US030952.	QY	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
PR	10-NOV-2000;	2000WO-US030873.	Db	241	TGACCACTGAAGACCCAGGGGTGGCGCATCTCAAGGACTATTACAGATACAACTT	297
XX						
PA	(GETH) GENENTECH INC.					
XX	Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;					
PI	Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;					
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;					
XX						
DR	WPI: 2001-408281/43.					
DR	P-PSDB; AAU12438.					
XX						
PT	Isolated , secretory and transmembrane PRO polypeptide used to detect					
PT	other PRO polypeptides, link bioactive molecules to cells expressing PRO					
PT	polypeptides, and detect the presence of mammalian tumors e.g. lung,					
PT	breast, prostate, cervical.					
XX						
PS	Claim 3; Fig 533; 813pp; English.					
XX						
CC	AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO					
CC	polypeptides. The PRO polypeptides are useful to detect other PRO					
CC	polypeptides, to link bioactive molecules to cells expressing PRO					
CC	polypeptides, to modulate biological activities of cells expressing PRO					
CC	polypeptides, and to detect the presence of mammalian lung, colon,					
CC	breast, prostate, rectal, cervical or liver tumours by comparing PRO					
CC	polypeptide expression in a cell sample to that in a control sample. Some					
CC	of the 275 sequences are also useful to stimulate the release of tumour					
CC	necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or					
CC	differentiation of chondrocytes, the proliferation or gene expression in					
CC	pericyte cells, the release of proteoglycans from cartilage, the					
CC	proliferation of inner ear utricular supporting cells or of T-					
CC	lymphocytes, the release of a cytokine from peripheral blood monocytes					
CC	(PBMCs), or the proliferation of endothelial cells. Some of the PRO					
CC	polypeptides may modulate glucose or free fatty acid uptake by skeletal					
CC	muscle cells or by adipocytes; or inhibit binding of A-peptide to factor					
CC	VIIA. The PRO polypeptides can be used in assays to identify molecules					
CC	involved in binding interactions. The polynucleotides encoding PRO					
CC	polypeptides can be used to generate probes, antisense RNA/DNA,					
CC	transgenic or knock out animals and can be used in gene therapy					
XX						
SQ	Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;					
XX						
QY	Query Match 48.0%; Score 284.2; DB 4; Length 496;					
	Best Local Similarity 97.3%; Pred. No. 1.9e-66;					
	Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;					
QY	1 TCTGCTCCACTGCTCTGCTGGGATCATGGAACCTTGACACTGCTGCTGGGCTGGTGGT					60

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PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 23-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-00886342.
PR 21-JUN-2001; 2001WO-US019692.
PR 22-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001US-00921735.
PR 18-JUL-2001; 2001US-00908927.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.

PR 19-DEC-2001; 2001US-00028072.
PR (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-341980/32.
DR P-PSDB; ABO17882.
XX
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 2; Fig 533; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression.
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide
XX
SQ Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;

Query Match 48.0%; Score 284.2; DB 7; Length 496;
Best Local Similarity 97.3%; Pred. No. 1.9e-66;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TCTGCTCCACTGCTGTGTGGGATCATGGAATTCGACTGCTGTGGCTGGTGGT 60
Db |||||
QY 1 TCTGCTCCACTGCTGTGTGGGATCATGGAATTCGACTGCTGTGGCTGGTGGT 60
Db |||||
QY 61 GATGGCTGGTGTGATTCGAATCCAGGGCGGGATCCTGAACCTGAACAGATGGTCAAGCA 120
Db |||||
QY 61 GATGGCTGGTGTGATTCGAATCCAGGGCGGGATCCTGAACCTGAACAGATGGTCAAGCA 120
Db |||||
QY 121 AGTGACTGGGAAAATGCCATCTCTCTACTGCGCCCTACGGCTGTCACTCGGACTAGG 180
Db |||||
QY 121 AGTGACTGGGAAAATGCCATCTCTCTACTGCGCCCTACGGCTGTCACTCGGACTAGG 180
Db |||||
QY 181 TGGCAGAGGGCCCAACCCAAAGATGCCAGGACTGTGTGTCCAGACCCATGACTCTGCTA 240
Db |||||
QY 181 TGGCAGAGGGCCCAACCCAAAGATGCCAGGACTGTGTGTCCAGACCCATGACTCTGCTA 240
Db |||||
QY 241 TGACCACTTGAGACCCAGGGGTGGCGCATCTTACAAGGACTATTACAGATACACTT 297
Db |||||
QY 241 TGACCACTTGAGACCCAGGGGTGGCGCATCTTACAAGGACTATTACAGATACACTT 297
Db |||||

RESULT 14
ACA67260
ID ACA67260 standard; cDNA; 496 BP.
XX
AC ACA67260;

```

[illegible]

CC serum, and for affinity purification of PRO from recombinant cell culture
 CC or natural sources. ACA6994-ACA67268 represent cDNA sequences encoding
 CC the human PRO polypeptides of the invention. Note: The sequence data for
 CC this patent was obtained in electronic format directly from the USPTO web
 CC site at seqdata.uspto.gov/psipsdIDEntry.html
 XX
 SQ Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;

Query Match 48.0%; Score 284.2; DB 7; Length 496;
 Best Local Similarity 97.3%; Pred. No. 1.9e-66;
 Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TCTGCTCCACCTCTGCTGGGATCATGGAACCTGCACTGTGGGCTGTGGT 60
 Db 1 TCTGCTCCACCTCTGTGCTGGGATCATGGAACCTGCACTGTGGGCTGTGGT 60
 QY 61 GATGGCTGGTGTGATTCCTCAATCCAGGCGGGATCTTGAACCTGAAAGATGTCGAAGCA 120
 Db 61 GATGGCTGGTGTGATTCCTCAATCCAGGCGGGATCTTGAACCTGAAAGATGTCGAAGCA 120
 QY 121 AGTGACTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGCCGACTAGG 180
 Db 121 AGTGACTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGCCGACTAGG 180
 QY 181 TGGCAGAGCCCAACCAAGATGCCACGACTGGTCTGCCAGACCCATGACTGTGCTA 240
 Db 181 TGGCAGAGCCCAACCAAGATGCCACGACTGGTCTGCCAGACCCATGACTGTGCTA 240
 QY 241 TGACCACTGAAGACCCAGGGGTGGGATCTTCAAGGACTATTACAGATCAACTT 297
 Db 241 TGACCACTGAAGACCCAGGGGTGGGATCTTCAAGGACTATTACAGATCAACTT 297

RESULT 15

ACA03869
 ID ACA03869 standard; cDNA; 496 BP.

XX AC ACA03869;

XX DT 23-MAY-2003 (first entry)

XX DE cDNA encoding human PRO polypeptide #267.

XX KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
 KW ss.

XX OS Homo sapiens.

XX PN US2003036180-A1.

XX PD 20-FEB-2003.

XX PF 09-MAY-2002; 2002US-00143114.

XX PP 31-MAR-1997; 97WO-US005230.

XX PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 14-SEP-1998; 98WO-US019094.

PR 16-SEP-1998; 98WO-US019177.

PR 17-SEP-1998; 98WO-US019330.

PR 07-OCT-1998; 98WO-US019437.

PR 29-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022991.

PR 29-OCT-1998; 98WO-US022992.

PR 01-DEC-1998; 98WO-US024855.

PR 05-JAN-1999; 98WO-US025108.

PR 08-MAR-1999; 98WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US0008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US028565.
 PR 20-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 22-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 05-JAN-2000; 99WO-US031274.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 11-FEB-2000; 2000WO-US000376.
 PR 18-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 10-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006319.
 PR 20-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US007532.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US014941.
 PR 28-JUL-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US020710.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023522.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001US-00796498.
 PR 01-MAR-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001WO-US006520.
 PR 14-MAR-2001; 2001US-00802706.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00828366.
 PR 18-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-0086028.
 PR 25-MAY-2001; 2001US-0086028.
 PR 25-MAY-2001; 2001US-0086028.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00874503.
 PR 19-JUN-2001; 2001US-00882636.
 PR 20-JUN-2001; 2001US-00882636.
 PR 20-JUN-2001; 2001WO-US019692.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, and for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The PRO polypeptides are useful for stimulating the release of tumor necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumors. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at serdata.uspto.gov/pa/paSPIDEntry.html

Search completed: October 7, 2004, 13:34:27
Job time : 258.748 secs

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	119.6	20.2	1016	4	US-09-220-132-17	Sequence 17, Appl
2	118	19.9	1014	2	US-08-888-497-31	Sequence 31, Appl
3	118	19.9	1014	2	US-09-362-230-31	Sequence 31, Appl
4	118	19.9	1014	5	PCT-US94-07926-31	Sequence 31, Appl
5	112.4	19.0	479	1	US-08-186-895-9	Sequence 9, Appl
6	110.8	18.7	854	4	US-09-023-655-1207	Sequence 1207, Appl
7	101.8	17.2	375	4	US-08-740-569-1	Sequence 1, Appl
8	98.4	16.6	1828	2	US-08-888-497-29	Sequence 29, Appl
9	98.4	16.6	1828	4	US-09-362-230-29	Sequence 29, Appl
10	98.4	16.6	1828	5	PCT-US94-07926-29	Sequence 29, Appl
11	92.6	15.6	4325	2	US-08-888-497-21	Sequence 21, Appl
12	92.6	15.6	4325	4	US-09-362-230-21	Sequence 21, Appl
13	92.6	15.6	4325	5	PCT-US94-07926-21	Sequence 21, Appl
14	63.2	10.7	742	3	US-08-966-317-2	Sequence 2, Appl
15	63.2	10.7	742	4	US-09-489-770-2	Sequence 2, Appl
16	62.6	10.6	562	4	US-09-023-655-1200	Sequence 1200, Appl
17	52.6	8.9	15328	2	US-08-888-497-13	Sequence 33, Appl
18	52.6	8.9	15328	4	US-09-362-230-33	Sequence 33, Appl
19	52.6	8.9	15328	5	PCT-US94-07926-33	Sequence 33, Appl
20	51	8.6	151	2	US-08-888-497-26	Sequence 26, Appl
21	51	8.6	151	4	US-09-362-230-26	Sequence 26, Appl
22	51	8.6	151	5	PCT-US94-07926-26	Sequence 26, Appl
23	50.4	8.5	151	2	US-08-888-497-25	Sequence 25, Appl
24	50.4	8.5	151	4	US-09-362-230-25	Sequence 25, Appl
25	50.4	8.5	151	5	PCT-US94-07926-25	Sequence 25, Appl
26	38.2	6.5	167	2	US-08-888-497-28	Sequence 28, Appl
27	38.2	6.5	167	4	US-09-362-230-28	Sequence 28, Appl


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Best Local Similarity 57.8%; Pred. No. 2.8e-23;
Matches 230; Conservative 0; Mismatches 165; Indels 3; Gaps 1;

QY 67 TGTGTGATCCCAATCCAGGCGGGATCCCTGAACCTGAACAGATGTCAGCAAGTGAC 126
Db 169 TAGTGTGCTGCTGTGCAAGAGGCTTGTGGACCTAAATCAATGATCAGAAAGTGAC 228
QY 127 TGGGAATAATGCCATCCTCTCTACTGGCCCTACGGCTGTCACTGCGGACTAGTGGCAG 186
Db 229 AGGGAAGAACGCCCTGACAAACTACGGCTGTCTAGGCTGTACTGCGGCTGGGGCGCG 288
QY 187 AGGCCAACCAAGATGCCAGGACTGTGCTGTCAGACCCATGCTGTGCTATGACCA 246
Db 289 AGGAACCCCAAGATGGCAAGGCTTGTGGACCTTGTGGCGCATGACCACTGTATGGCG 348
QY 247 CTGAAGACCCAGGGTGGCGCATCTACAAGGACTATTACAGATACAACTTTTCCAGG 306
Db 349 GCTGGAGGAGAGGGCTGCAACATTCGCAACAGTCTCAAAATACAGATTCGCGTGGG 408
QY 307 GAACATCCACTGTCTGAACAAGGAAGCTGGTGTGAGCAGCAGCTGTGTGCTGTGACAA 366
Db 409 CGTGTGCTACCTGC---GAGCCCGGGCCCTTCTGCCATGTCAACTCTGTGCTGTGACCG 465
QY 367 GGAGGTGGCTTCTGCTGAAGCGCAACCTGGACACTTACCAAGGAGCTGCGTTTCTA 426
Db 466 GAAGCTGCTACTGTCTCAAGAGAAACCTACGAGCTACAAACCAAGTACCAATATT 525
QY 427 CTGGCGGCCCACTGCGGGGGCAGACCCCTGGTGTCT 464
Db 526 TCCCAACATCCTCTGCTCTAGGCTTCCCGAGGAGCT 563

RESULT 4
PCT-US94-07926-31
; Sequence 31, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1014 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..544
PCT-US94-07926-31

Query Match 19.9%; Score 118; DB 5; Length 1014;
Best Local Similarity 57.8%; Pred. No. 2.8e-23;
Matches 230; Conservative 0; Mismatches 165; Indels 3; Gaps 1;

QY 67 TGTGTGATCCCAATCCAGGCGGGATCCCTGAACCTGAACAGATGTCAGCAAGTGAC 126
Db 169 TAGTGTGCTGCTGTGCAAGAGGCTTGTGGACCTTGTGGCGCATGACCACTGTATGGCG 228
QY 127 TGGGAATAATGCCATCCTCTCTACTGGCCCTACGGCTGTCACTGCGGACTAGTGGCAG 186
Db 229 AGGGAAGAACGCCCTGACAAACTACGGCTGTCTAGGCTGTACTGCGGCTGGGGCGCG 288
QY 187 AGGCCAACCAAGATGCCAGGACTGTGCTGTCAGACCCATGCTGTGCTATGACCA 246
Db 289 AGGAACCCCAAGATGGCAAGGCTTGTGGACCTTGTGGCGCATGACCACTGTATGGCG 348
QY 247 CTGAAGACCCAGGGTGGCGCATCTACAAGGACTATTACAGATACAACTTTTCCAGG 306
Db 349 GCTGGAGGAGAGGGCTGCAACATTCGCAACAGTCTCAAAATACAGATTCGCGTGGG 408
QY 307 GAACATCCACTGTCTGAACAAGGAAGCTGGTGTGAGCAGCAGCTGTGTGCTGTGACAA 366
Db 409 CGTGTGCTACCTGC---GAGCCCGGGCCCTTCTGCCATGTCAACTCTGTGCTGTGACCG 465
QY 367 GGAGGTGGCTTCTGCTGAAGCGCAACCTGGACACTTACCAAGGAGCTGCGTTTCTA 426
Db 466 GAAGCTGCTACTGTCTCAAGAGAAACCTACGAGCTACAAACCAAGTACCAATATT 525
QY 427 CTGGCGGCCCACTGCGGGGGCAGACCCCTGGTGTCT 464
Db 526 TCCCAACATCCTCTGCTCTAGGCTTCCCGAGGAGCT 563

RESULT 5
US-08-186-895-9
; Sequence 9, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
; APPLICANT: Hollis, Melvyn
; APPLICANT: Needham, Maurice R.C.
; APPLICANT: Gooding, Clare
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: Expression Systems
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,895
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,383
; FILING DATE: 09-APR-1993
; APPLICATION NUMBER: US/07/810,414

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Fri Oct 8 10:22:35 2004

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
 ADDRESSEE: Russell PA
 STREET: 200 East Broward Boulevard
 CITY: Fort Lauderdale
 STATE: FL
 COUNTRY: USA
 ZIP: 33301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/362,230
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/888,497
 FILING DATE:
 APPLICATION NUMBER: US 08/097,354
 FILING DATE: 26-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: IN21044-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-527-2498
 TELEFAX: 305-764-4996
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1828 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 233..643
 US-09-362-230-29

Query Match 16.6%; Score 98.4; DB 4; Length 1828;
 Best Local Similarity 57.6%; Pred. No. 9e-18;
 Matches 196; Conservative 0; Mismatches 141; Indels 3; Gaps 1;
 QY 69 GTGTGATTCCTCAATCCAGGCGGGATCCTGAACTGAACCAAGATGCTCAAGCAAGTCACTG 128
 Db 273 GTGTGCTCGAGTCCAGGGGGCTTGCTAGAACTGAAGTCCATGATTGAGAAGGTGACTG 332
 QY 129 GGAATATGCCATTCCTCTACTGSCCTTACGGCTGCTCACTGCGGACTAGGTGGCAGAG 188
 Db 333 GGAAGAAATGCGGFAAAGAACTATGGCTTCTACGGCTGCTACTGTGCTGGGGCGGCAG 392
 QY 189 GCCAACCCCAAGATGCCAGGACTGTGCTGCGAGACCCATGACTGCTGCTATGACACACC 248
 Db 393 GGACCCCTAAGATGGCACTGATTGGTGTGCTGGATGACGACCGTGTATATGGGTAC 452
 QY 249 TGAAGACCCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACTTTTCCAGGGGA 308
 Db 453 TGGAGGAGAAACACTGTGCCATCCGACCCAGTCTATGACTACAGATTACACACAGG-- 509
 QY 309 ACATCCACTCTGTGACAGGAGCTGGTGTGAGCAGAGCTGTGCTGTGCTGTGCTGTGCTG 368
 Db 510 ACTTAGTCACTCTGCAACACGACTCTCTTCTGTCAGTAGGCTTTGCTGTGACCGGA 569
 QY 369 AGGTGGGCTTCTGCTCAAGCGCAACCTGGACACCTACCA 408
 Db 570 AGCTGGTCTACTGCTGAGGAGAACTCTGAGATTACAA 609

RESULT 10
 PCT-US94-07926-29
 ; Sequence 29, Application PC/TUS9407926

GENERAL INFORMATION:
 APPLICANT: Tischnfield, Jay A.
 APPLICANT: Seilhamer, Jeffrey J.
 TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
 TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
 TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
 TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
 ADDRESSEE: Russell PA
 STREET: 200 East Broward Boulevard
 CITY: Fort Lauderdale
 STATE: FL
 COUNTRY: USA
 ZIP: 33301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/07926
 FILING DATE: 15-JUL-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/097,354
 FILING DATE: 26-JUL-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: IN21044-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305-527-2498
 TELEFAX: 305-764-4996
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1828 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 233..643
 PCT-US94-07926-29

Query Match 16.6%; Score 98.4; DB 5; Length 1828;
 Best Local Similarity 57.6%; Pred. No. 9e-18;
 Matches 196; Conservative 0; Mismatches 141; Indels 3; Gaps 1;
 QY 69 GTGTGATTCCTCAATCCAGGCGGGATCCTGAACTGAACCAAGATGCTCAAGCAAGTCACTG 128
 Db 273 GTGTGCTCGAGTCCAGGGGGCTTGCTAGAACTGAAGTCCATGATTGAGAAGGTGACTG 332
 QY 129 GGAATATGCCATTCCTCTACTGSCCTTACGGCTGCTCACTGCGGACTAGGTGGCAGAG 188
 Db 333 GGAAGAAATGCGGFAAAGAACTATGGCTTCTACGGCTGCTACTGTGCTGGGGCGGCAG 392
 QY 189 GCCAACCCCAAGATGCCAGGACTGTGCTGCGAGACCCATGACTGCTGCTATGACACACC 248
 Db 393 GGACCCCTAAGATGGCACTGATTGGTGTGCTGGATGACGACCGTGTATATGGGTAC 452
 QY 249 TGAAGACCCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACTTTTCCAGGGGA 308
 Db 453 TGGAGGAGAAACACTGTGCCATCCGACCCAGTCTATGACTACAGATTACACACAGG-- 509
 QY 309 ACATCCACTCTGTGACAGGAGCTGGTGTGAGCAGAGCTGTGCTGTGCTGTGCTGTGCTG 368
 Db 510 ACTTAGTCACTCTGCAACACGACTCTCTTCTGTCAGTAGGCTTTGCTGTGACCGGA 569
 QY 369 AGGTGGGCTTCTGCTCAAGCGCAACCTGGACACCTACCA 408

Db 570 AGCTGGTCTACTGCTGAGGAGAAACCTCTGGAGTTACAA 609

RESULT 11
US-08-888-497-21
; Sequence 21, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,497
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,405
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 722..1195
US-08-888-497-21

Query Match 15.6%; Score 92.6; DB 2; Length 4325;
Best Local Similarity 56.9%; Pred. No. 4.9e-16;
Matches 195; Conservative 0; Mismatches 139; Indels 9; Gaps 1;

Qy 78 CAATCCAGGGGGGATCTCTGAACCTGAAGAGTGGTCAAGCAAGTGAAGTGGGAAATGC 137
Db 795 CCACCTCAGCAGCTTCTGGCAGTGTCCAGAGATGGTCAACACATCAGGGGCGCAGCG 854

Qy 138 CCATCTCTCTACTGCGCCCTACGCTGCTACTGCGGACTAGGTGGGAGAGGCCCAACCCA 197
Db 855 CTTCTCTCTCTATACGATATGCTGCTACTGTGGGCTTGGGGCGCGAGGATCCCTG 914

Qy 198 AAGATGCCACGAGTGGTGTGCGCAGACCCATGCTGCTGTATGACCACTGAAGACCC 257
Db 915 TGGACGCCACAGACAGGTGCTGCTGGGCTCATGCTGTGTGTACACAGCTTAAAGAA 974

Qy 258 AGGGGTGGGGCATCTACAAAGGACTATTACAGATACAACTTTTCCAGGGGAAATCCACT 317

Db 975 ATGGCTGCCAGCCCATCTTGAATGCCATATCAGTTTGCATTTGCAACGGGACCGTGACCT 1034
Qy 318 G-----CTCTGACAAAGGAAAGCTGGTGTGAGCAGCAGCTGTGTGCTGTGACAAAGG 368
Db 1035 GTGGATGCACCATGGGTGGCGGCTGCTTGTGCGGGCAGAAAGCTGTGAGTGTGACAAAC 1094

Qy 369 AGTGGCTTCTCCCTGAAGCGCAACCTGGACACCTTACCAGAA 411
Db 1095 TGTCTGTGTAAGCTTCAAGGAGAACCTGGCCACCTTACCAGAA 1137

RESULT 12
US-09-362-230-21
; Sequence 21, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/362,230
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/888,497
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 722..1195
US-09-362-230-21

Query Match 15.6%; Score 92.6; DB 4; Length 4325;
Best Local Similarity 56.9%; Pred. No. 4.9e-16;
Matches 195; Conservative 0; Mismatches 139; Indels 9; Gaps 1;

Qy 78 CAATCCAGGGGGGATCTCTGAACCTGAAGAGTGGTCAAGCAAGTGAAGTGGGAAATGC 137
Db 795 CCACCTCAGCAGCTTCTGGCAGTGTCCAGAGATGGTCAACACATCAGGGGCGCAGCG 854

US-09-489-770-2

Query Match	10.7%;	Score 63.2;	DB 4;	Length 742;
Best Local Similarity	51.8%;	Pred. No. 3.5e-08;		
Matches 143;	Conservative 0;	Mismatches 133;	Indels 0;	Gaps 0;
QY	138	CCATCCTCTCCTACTGGCCCTACGGCTGTCACTTCGGGACTAGTGTGGCAGAGGCCAACCCCA	197	
Db	197	CCCCCATCGCTATATCAAAATATGGTTGCTTTTGTGGCTTTGGGAGGCCATGGCCAGCCCC	256	
QY	198	AAGATCCACGGACTGGTGTCCGACACCATCACTCTGTATGACCACTGTAAGACCC	257	
Db	257	GCATGCCCATTTGACTGGTGTCTGCATGGCCACGACTGTTGTACACTCGAGCTGAGGAGG	316	
QY	258	AGGGGTGGGCATCTACAAGGACTATTACAGATACAACATTTTCCAGGGGAAACATCCACT	317	
Db	317	CCGGCTGCAGCCCCAGACAGAGCGGTACTTCCTGGCAGTCGCTCAATCAGAGCGTCTCGT	376	
QY	318	GCTCTGACAAGGAAAGCTGGTGTGACGACGAGCTGTGTGCTGTGACCAAGAGAGTGGCCCT	377	
Db	377	GGGACCGGCAGAGACAATGCCAGAAGCTGTTGTCAAGTGTGACCGAGAGATTGCTA	436	
QY	378	TTTGCTGAAGGCACACCTGGACACCTACCAGAAGC	413	
Db	437	ACTGCTTAGCCAAACTGAGTGACAACTTAAAGTACC	472	

Search completed: October 7, 2004, 18:59:22
Job time : 49.7926 secs

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1	575.4	97.2	854	9	US-09-969-384-6	Sequence 6, Appli
2	568.8	96.1	1927	13	US-10-236-115-603	Sequence 603, App
3	567.4	95.8	1931	9	US-09-835-996A-5	Sequence 5, Appli
4	284.2	48.0	496	10	US-09-946-374-377	Sequence 377, App
5	284.2	48.0	496	12	US-10-015-395A-377	Sequence 377, App
6	284.2	48.0	496	13	US-10-147-493-533	Sequence 533, App
7	284.2	48.0	496	12	US-10-145-127-533	Sequence 533, App
8	284.2	48.0	496	13	US-10-160-503-533	Sequence 533, App
9	284.2	48.0	496	13	US-10-143-118-533	Sequence 533, App
10	284.2	48.0	496	13	US-10-144-993-533	Sequence 533, App
11	284.2	48.0	496	13	US-10-158-787-533	Sequence 533, App
12	284.2	48.0	496	13	US-10-140-024-533	Sequence 533, App
13	284.2	48.0	496	13	US-10-140-808-533	Sequence 533, App
14	284.2	48.0	496	13	US-10-006-485A-377	Sequence 377, App


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RESULT 4
US-09-946-374-377
; Sequence 377, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Tr
; FILE REFERENCE: Acids Encoding
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/9-
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716

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PRIOR APPLICATION NUMBER: 60/101068	PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101071	PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101072	PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101279	PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101471	PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101472	PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101474	PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101475	PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101476	PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101477	PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101479	PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738	PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741	PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743	PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101915	PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916	PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102207	PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102240	PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102307	PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102330	PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102331	PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102484	PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102487	PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102570	PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102571	PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102684	PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102687	PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965	PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258	PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314	PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315	PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328	PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103395	PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103396	PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103401	PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103449	PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103633	PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103678	

✓	PRIOR FILING DATE:	1998-10-08
✓	PRIOR APPLICATION NUMBER:	60/103679
✓	PRIOR FILING DATE:	1998-10-08
✓	PRIOR APPLICATION NUMBER:	60/103711
✓	PRIOR FILING DATE:	1998-10-08
✓	PRIOR APPLICATION NUMBER:	60/104257
✓	PRIOR FILING DATE:	1998-10-14
✓	PRIOR APPLICATION NUMBER:	60/104987
✓	PRIOR FILING DATE:	1998-10-20
✓	PRIOR APPLICATION NUMBER:	60/105000
✓	PRIOR FILING DATE:	1998-10-20
✓	PRIOR APPLICATION NUMBER:	60/105002
✓	PRIOR FILING DATE:	1998-10-20
✓	PRIOR APPLICATION NUMBER:	60/105104
✓	PRIOR FILING DATE:	1998-10-21
✓	PRIOR APPLICATION NUMBER:	60/105169
✓	PRIOR FILING DATE:	1998-10-22
✓	PRIOR APPLICATION NUMBER:	60/105266
✓	PRIOR FILING DATE:	1998-10-22
✓	PRIOR APPLICATION NUMBER:	60/105693
✓	PRIOR FILING DATE:	1998-10-26
✓	PRIOR APPLICATION NUMBER:	60/105694
✓	PRIOR FILING DATE:	1998-10-26
✓	PRIOR APPLICATION NUMBER:	60/105807

Query Match	48.0%;	Score 284.2;	DB 10;	Length 496;
Best Local Similarity	97.3%;	Pred. No. 4.4e-79;		
Matches 289;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
QY	1	TCTGCCTCCACTGCTCTGCTGGGATCATGGAATTGCAC	TGCTGTGCTGTGGCTGGTGGT	60
Db				
QY	1	TCTGCCTCCACTGCTCTGCTGGGATCATGGAATTGCAC	TGCTGTGCTGTGGGCTGGTGGT	60
Db				
QY	61	GATGGCTGCTGTGATTCCAAATCCAGGGGGGATCCTGAAC	CTGAAAGATGGTCAAGCA	120
Db				
QY	61	GATGGCTGCTGTGATTCCAAATCCAGGGGGGATCCTGAAC	CTGAAAGATGGTCAAGCA	120
Db				
QY	121	AGTGACTGGGAAAAATGCCATCCTCTCTACTTGGCCCT	TACGGCTGTCACTCGGGACTAGG	180
Db				
QY	121	AGTGACTGGGAAAAATGCCATCCTCTCTACTTGGCCCT	TACGGCTGTCACTCGGGACTAGG	180
Db				
QY	181	TGGCAGAGGGCCAAACCCAAAGATGCCAGGATGGTGTG	TGTCAGACCCATGACTGTGCTA	240
Db				
QY	181	TGGCAGAGGGCCAAACCCAAAGATGCCAGGATGGTGTG	TGTCAGACCCATGACTGTGCTA	240
Db				
QY	241	TGACCACTGAGACCCAGGGTGGCGATCTCAAGGACTATT	PACAGATACAACTT	297
Db				
QY	241	TGACCACTGAGACCCAGGGTGGCGATCTCAAGGACTATT	PACAGATACAACTT	297
Db				

```

RESULT 5
US-10-015-395A-377
; Sequence 377, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC57
; CURRENT APPLICATION NUMBER: US/10/015.395A

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; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 377
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-015-395A-377

Query Match 48.0%; Score 284.2; DB 12; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TCTGCTCCACTGCTCTGTGCTGGGATCATGGAACCTTGCACTGCTGTGGGCTGGT 60
DB 1 TCTGCTCCACTGCTCTGTGCTGGGATCATGGAACCTTGCACTGCTGTGGGCTGGT 60

QY 61 GATGGCTGGTGTGATTCCTCAATCCAGGCGGGATCCTGAACTTGAACATGATGTCAGCA 120
DB 61 GATGGCTGGTGTGATTCCTCAATCCAGGCGGGATCCTGAACTTGAACATGATGTCAGCA 120

QY 121 AGTACTGGGAAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180
DB 121 AGTACTGGGAAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180

QY 181 TGGCAGAGCCCAACCCAAAGATGCCAGGACTGGTGTGCCAGACCCATGCTGTGCTA 240
DB 181 TGGCAGAGCCCAACCCAAAGATGCCAGGACTGGTGTGCCAGACCCATGCTGTGCTA 240

QY 241 TGACCACTTGAGACCCAGGGGTGGGCATCTACAGGACTATTACAGATACACTT 297
DB 241 TGACCACTTGAGACCCAGGGGTGGGCATCTACAGGACTATTACAGATACACTT 297

RESULT 6

US-10-147-493-533
; Sequence 533, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure

; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-147-493-533

Query Match 48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TCTGCTCCACTGCTCTGTGCTGGGATCATGGAACCTTGCACTGCTGTGGGCTGGT 60
DB 1 TCTGCTCCACTGCTCTGTGCTGGGATCATGGAACCTTGCACTGCTGTGGGCTGGT 60

QY 61 GATGGCTGGTGTGATTCCTCAATCCAGGCGGGATCCTGAACTTGAACATGATGTCAGCA 120
DB 61 GATGGCTGGTGTGATTCCTCAATCCAGGCGGGATCCTGAACTTGAACATGATGTCAGCA 120

QY 121 AGTACTGGGAAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180
DB 121 AGTACTGGGAAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180

QY 181 TGGCAGAGCCCAACCCAAAGATGCCAGGACTGGTGTGCCAGACCCATGCTGTGCTA 240
DB 181 TGGCAGAGCCCAACCCAAAGATGCCAGGACTGGTGTGCCAGACCCATGCTGTGCTA 240

QY 241 TGACCACTTGAGACCCAGGGGTGGGCATCTACAGGACTATTACAGATACACTT 297
DB 241 TGACCACTTGAGACCCAGGGGTGGGCATCTACAGGACTATTACAGATACACTT 297

RESULT 7

US-10-145-127-533
; Sequence 533, Application US/10145127
; Publication No. US20040033558A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C252
; CURRENT APPLICATION NUMBER: US/10/145,127
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-145-127-533

Query Match 48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TCTGCTCCACTGCTCTGTGCTGGGATCATGGAACCTTGCACTGCTGTGGGCTGGT 60

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Db 1 TCTGCTCCACTGCTGCTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
QY 61 GATGGCTGGTGTGATTCCAATCCAGGCGGGATCTGGAACCTGGAACAGATGGTCAAGCA 120
Db 61 GATGGCTGGTGTGATTCCAATCCAGGCGGGATCTGGAACCTGGAACAGATGGTCAAGCA 120
QY 121 AGTGAAGTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180
Db 121 AGTGAAGTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180
QY 181 TGGCAGAGGCCCAACCCAAAGATGCCAGGATGGTGTGCTGCCAGACCCATGCTGTGCTA 240
Db 181 TGGCAGAGGCCCAACCCAAAGATGCCAGGATGGTGTGCTGCCAGACCCATGCTGTGCTA 240
QY 241 TGACCACCTGAAGACCCAGGGGTGGGCATCTTACAGGACTATTACAGATACAACCTT 297
Db 241 TGACCACCTGAAGACCCAGGGGTGGGCATCTTACAGGACTATTACAGATACAACCTT 297
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RESULT 8

US-10-160-503-533

; Sequence 533, Application US/10160503

; Publication No. US20040033559A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C446

; CURRENT APPLICATION NUMBER: US/10/160,503

; CURRENT FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 533

; LENGTH: 496

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 396

; OTHER INFORMATION: unknown base

US-10-160-503-533

Query Match 48.0%; Score 284.2; DB 13; Length 496;

Best Local Similarity 97.3%; Pred. No. 4.4e-79;

Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1 TCTGCTCCACTGCTGCTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
Db 1 TCTGCTCCACTGCTGCTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT 60
QY 61 GATGGCTGGTGTGATTCCAATCCAGGCGGGATCTGGAACCTGGAACAGATGGTCAAGCA 120
Db 61 GATGGCTGGTGTGATTCCAATCCAGGCGGGATCTGGAACCTGGAACAGATGGTCAAGCA 120
QY 121 AGTGAAGTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180
Db 121 AGTGAAGTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180
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RESULT 10

US-10-144-993-533
; Sequence 533, Application US/10144993
; Publication No. US20040038336A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC261

; CURRENT APPLICATION NUMBER: US/10/144,993
; CURRENT FILING DATE: 2002-05-13

; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 533
; LENGTH: 496

; TYPE: DNA
; ORGANISM: Homo Sapien

; FEATURE:
; NAME/KEY: unsure

; LOCATION: 396
; OTHER INFORMATION: unknown base

US-10-144-993-533

Query Match 48.0%; Score 284.2; DB 13; Length 496;

Best Local Similarity 97.3%; Pred. No. 4.4e-79;

Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TCTGCTCCACTGCTGTGGGATCATGGAACCTTGCACTGCTGTGGGCTGTGGT 60

Db 1 TCTGCTCCACTGCTGTGGGATCATGGAACCTTGCACTGCTGTGGGCTGTGGT 60

QY 61 GATGCTGGTGTGATTCCCAATCCAGGCGGGATCCTGAACTGAAACAGATGTCACGCA 120

Db 61 GATGCTGGTGTGATTCCCAATCCAGGCGGGATCCTGAACTGAAACAGATGTCACGCA 120

QY 121 AGTGACTGGGAAATGCCCAATCCAGGCGGGATCCTGAACTGAAACAGATGTCACGCA 180

Db 121 AGTGACTGGGAAATGCCCAATCCAGGCGGGATCCTGAACTGAAACAGATGTCACGCA 180

QY 181 TGGCAGAGCCCAACCAAGATGCCAGGCTGTGGCTGCCAGACCCATGCTGTGCTA 240

Db 181 TGGCAGAGCCCAACCAAGATGCCAGGCTGTGGCTGCCAGACCCATGCTGTGCTA 240

QY 241 TGACCACTGAAGACCCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACCTT 297

Db 241 TGACCACTGAAGACCCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACCTT 297

RESULT 11

US-10-158-787-533

; Sequence 533, Application US/10158787
; Publication No. US20040039164A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC449

; CURRENT APPLICATION NUMBER: US/10/158,787
; CURRENT FILING DATE: 2003-04-03

; Prior Application Number: 60/049911
; Prior Filing Date: 1997-06-18

; Prior Application Number: 60/056974
; Prior Filing Date: 1997-08-26

; Prior Application Number: 60/059113
; Prior Filing Date: 1997-09-17

; Prior Application Number: 60/059115
; Prior Filing Date: 1997-09-17

; Prior Application Number: 60/059117
; Prior Filing Date: 1997-09-17

; Prior Application Number: 60/059122
; Prior Filing Date: 1997-09-17

; Prior Application Number: 60/059184
; Prior Filing Date: 1997-09-17

; Prior Application Number: 60/059263
; Prior Filing Date: 1997-09-18

; Prior Application Number: 60/059352
; Prior Filing Date: 1997-09-19

; Prior Application Number: 60/059588
; Prior Filing Date: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 533
; LENGTH: 496

; TYPE: DNA
; ORGANISM: Homo Sapien

; FEATURE:
; NAME/KEY: unsure

; LOCATION: 396
; OTHER INFORMATION: unknown base

US-10-158-787-533

Query Match 48.0%; Score 284.2; DB 13; Length 496;

Best Local Similarity 97.3%; Pred. No. 4.4e-79;

Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TCTGCTCCACTGCTGTGGGATCATGGAACCTTGCACTGCTGTGGGCTGTGGT 60

Db 1 TCTGCTCCACTGCTGTGGGATCATGGAACCTTGCACTGCTGTGGGCTGTGGT 60

QY 61 GATGCTGGTGTGATTCCCAATCCAGGCGGGATCCTGAACTGAAACAGATGTCACGCA 120

Db 61 GATGCTGGTGTGATTCCCAATCCAGGCGGGATCCTGAACTGAAACAGATGTCACGCA 120

QY 121 AGTGACTGGGAAATGCCCAATCCAGGCGGGATCCTGAACTGAAACAGATGTCACGCA 180

Db 121 AGTGACTGGGAAATGCCCAATCCAGGCGGGATCCTGAACTGAAACAGATGTCACGCA 180

QY 181 TGGCAGAGCCCAACCAAGATGCCAGGCTGTGGCTGCCAGACCCATGCTGTGCTA 240

Db 181 TGGCAGAGCCCAACCAAGATGCCAGGCTGTGGCTGCCAGACCCATGCTGTGCTA 240

QY 241 TGACCACTGAAGACCCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACCTT 297

Db 241 TGACCACTGAAGACCCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACCTT 297

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Db      241 TGACCACCTGAAGACCAGGGGTGGGCATCTACAAGGACAAACAAGAGCAGCAT 297

RESULT 12
US-10-024-533
; Sequence 533, Application US/10140024
; Publication No. US20040058424A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C69
; CURRENT APPLICATION NUMBER: US/10/140,024
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-140-024-533

Query Match      48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 TCTGCTCCACTGCTGTGTGGGATCATGGAACCTTGCACTGCTGTGTGGGCTGGTGT 60
Db      1 TCTGCTCCACTGCTGTGTGGGATCATGGAACCTTGCACTGCTGTGTGGGCTGGTGT 60
QY      61 GATGGCTGTGTGATTCCAAATCCAGGGGGGATCTTGAACCTGAAACAGATGGTCAAGCA 120
Db      61 GATGGCTGTGTGATTCCAAATCCAGGGGGGATCTTGAACCTGAAACAGATGGTCAAGCA 120
QY      121 AGTGAAGTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180
Db      121 AGTGAAGTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180
QY      181 TGCCAGAGGCCCAACCCAAAGATGCCAGGACTGGTGTGCCAGAGCCCATGACTGTGCTA 240
Db      181 TGCCAGAGGCCCAACCCAAAGATGCCAGGACTGGTGTGCCAGAGCCCATGACTGTGCTA 240
QY      241 TGACCACCTGAAGACCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACATT 297
Db      241 TGACCACCTGAAGACCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACATT 297

RESULT 13
US-10-140-808-533
; Sequence 533, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

```

```

; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 533
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 396
; OTHER INFORMATION: unknown base
; US-10-140-808-533

Query Match      48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 TCTGCTCCACTGCTGTGTGGGATCATGGAACCTTGCACTGCTGTGTGGGCTGGTGT 60
Db      1 TCTGCTCCACTGCTGTGTGGGATCATGGAACCTTGCACTGCTGTGTGGGCTGGTGT 60
QY      61 GATGGCTGTGTGATTCCAAATCCAGGGGGGATCTTGAACCTGAAACAGATGGTCAAGCA 120
Db      61 GATGGCTGTGTGATTCCAAATCCAGGGGGGATCTTGAACCTGAAACAGATGGTCAAGCA 120
QY      121 AGTGAAGTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180
Db      121 AGTGAAGTGGGAAATGCCCATCTCTCTACTGGCCCTACGGCTGTCACTGGGACTAGG 180
QY      181 TGCCAGAGGCCCAACCCAAAGATGCCAGGACTGGTGTGCCAGAGCCCATGACTGTGCTA 240
Db      181 TGCCAGAGGCCCAACCCAAAGATGCCAGGACTGGTGTGCCAGAGCCCATGACTGTGCTA 240
QY      241 TGACCACCTGAAGACCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACATT 297
Db      241 TGACCACCTGAAGACCAGGGGTGGGCATCTACAAGGACTATTACAGATACAACATT 297

RESULT 14
US-10-006-485A-377
; Sequence 377, Application US/10006485A
; Publication No. US20030064062A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

```

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C9
CURRENT APPLICATION NUMBER: US/10/006,485A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
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PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
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PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103395

;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103396
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103401
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103449
;; PRIOR FILING DATE: 1998-10-06
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;; PRIOR FILING DATE: 1998-10-08
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;; PRIOR APPLICATION NUMBER: 60/104257
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;; PRIOR APPLICATION NUMBER: 60/105002
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;; PRIOR APPLICATION NUMBER: 60/105266
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;; PRIOR APPLICATION NUMBER: 60/105807
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105881
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;; PRIOR APPLICATION NUMBER: 60/105882
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/106023
;; PRIOR FILING DATE: 1998-10-28

Query Match 48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TCTGCTCCACTGCTCTGCTGGGATCATGGAATTCGAACTTGCATGCTGTGTGGCTGTGTGGT 60
Db 1 TCTGCTCCACTGCTCTGCTGGGATCATGGAATTCGAACTTGCATGCTGTGTGGCTGTGTGGT 60

QY 61 GATGCTGGTGTGATTCCAAATCCAGGGGGGATCCTGAACTTGAACCAAGATGGTCAAGCA 120
Db 61 GATGCTGGTGTGATTCCAAATCCAGGGGGGATCCTGAACTTGAACCAAGATGGTCAAGCA 120

QY 121 AGTGACTGGGAAATGCCCAATCCTCTACTGGCCCTACGGCTGTCTACTGGGACTAGG 180
Db 121 AGTGACTGGGAAATGCCCAATCCTCTACTGGCCCTACGGCTGTCTACTGGGACTAGG 180

QY 181 TGGCAGAGGCCCAACCCAAAGATGCCACGACTGTGTGCTGCCAGACCCATGCTGTGCTA 240
Db 181 TGGCAGAGGCCCAACCCAAAGATGCCACGACTGTGTGCTGCCAGACCCATGCTGTGCTA 240

QY 241 TGACCACCTGAAGACCCAGGGGTGGGCATCTACAAAGGACTATTACAGATACAACCTT 297
Db 241 TGACCACCTGAAGACCCAGGGGTGGGCATCTACAAAGGACTATTACAGATACAACCTT 297

RESULT 15
US-10-013-907A-377
; Sequence 377, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan I.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2830PLC34
;; CURRENT APPLICATION NUMBER: US/10/013,907A
;; PRIOR FILING DATE: 2001-12-10
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 377
;; LENGTH: 496
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: 396
;; OTHER INFORMATION: unknown base
US-10-013-907A-377

Query Match 48.0%; Score 284.2; DB 13; Length 496;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TCTGCTCCACTGCTCTGCTGGGATCATGGAATTCGAACTTGCATGCTGTGTGGCTGTGTGGT 60
Db 1 TCTGCTCCACTGCTCTGCTGGGATCATGGAATTCGAACTTGCATGCTGTGTGGCTGTGTGGT 60

QY 61 GATGCTGGTGTGATTCCAAATCCAGGGGGGATCCTGAACTTGAACCAAGATGGTCAAGCA 120
Db 61 GATGCTGGTGTGATTCCAAATCCAGGGGGGATCCTGAACTTGAACCAAGATGGTCAAGCA 120

QY 121 AGTGACTGGGAAATGCCCAATCCTCTACTGGCCCTACGGCTGTCTACTGGGACTAGG 180
Db 121 AGTGACTGGGAAATGCCCAATCCTCTACTGGCCCTACGGCTGTCTACTGGGACTAGG 180

QY 181 TGGCAGAGGCCCAACCCAAAGATGCCACGACTGTGTGCTGCCAGACCCATGCTGTGCTA 240
Db 181 TGGCAGAGGCCCAACCCAAAGATGCCACGACTGTGTGCTGCCAGACCCATGCTGTGCTA 240

QY 241 TGACCACCTGAAGACCCAGGGGTGGGCATCTACAAAGGACTATTACAGATACAACCTT 297
Db 241 TGACCACCTGAAGACCCAGGGGTGGGCATCTACAAAGGACTATTACAGATACAACCTT 297

Search completed: October 7, 2004, 22:40:42
Job time : 307.834 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2004, 11:14:15 ; Search time 937.252 Seconds
(without alignments)
9989.875 Million cell updates/sec

Title: US-09-830-321A-5
Perfect score: 2204
Sequence: 1 catggttggggcgcagaga.....actcatcaaaaaaaaaaaaaa 2204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*
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3: Geneseqn2000s:*
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6: Geneseqn2002s:*
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8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2202	99.9	2204	3	AA53270 Human pho
2	1816.8	82.4	3085	3	Aaz88757 Human PLA
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4	1816.8	82.4	3085	4	Aaf74999 Phospholi
5	1816.8	82.4	3085	4	Aaf75000 Phospholi
6	1816.8	82.4	3085	4	Aaf90489 Human pho
7	1816.8	82.4	3085	4	Aaf90488 Human pho
8	1806.2	82.0	2699	6	AA517363 CDNA enco
9	1806.2	82.0	2699	7	ABX11884 Human cDN
10	1806.2	82.0	4183	6	AA517362 Partial c
11	1806.2	82.0	4183	7	ABX11883 Human par
12	1788.8	81.2	1925	2	AAV34229 Human sec
13	1788.8	81.2	1925	7	ACD08100 CDNA enco
14	1777.8	80.7	1926	2	AAV34164 Human sec
15	1777.8	80.7	1926	7	ACD08035 CDNA enco
16	1676.6	76.1	1818	2	AAV34230 Human sec
17	1676.6	76.1	1818	7	ACD08101 CDNA enco
18	1432.2	65.0	3419	5	AA584341 DNA enco
19	1408.6	63.9	8517	3	Aaz88756 Human PLA
20	1408.6	63.9	8517	4	Aaf74998 Phospholi
21	1408.6	63.9	8517	4	Aaf90487 Human pho
22	1388.8	63.0	3068	5	AA570058 DNA enco
23	728.8	33.1	5241	5	AA570056 DNA enco

24	602	27.3	2409	6	AA36478 Human pho
25	602	27.3	3138	9	AD10173 Human NOV
26	602	27.3	3197	6	AB94700 Human lip
27	602	27.3	3587	8	ADB6164 Human DNA
28	539.4	24.5	4499	5	AA584340 DNA enco
29	483.8	22.0	1915	4	AA534883 cDNA enco
30	483.8	22.0	1915	9	ADC46041 Human neo
31	451.4	20.5	567	5	AA584337 DNA enco
32	439	19.9	494	8	ACH45352 Human foe
33	429.6	19.5	3879	6	ABV72127 Nucleotid
34	415.6	18.9	4049	9	AD93423 Human lip
35	398.2	18.1	3418	9	ADE07210 Novel cod
36	398.2	18.1	3460	6	ABL51334 Human pho
37	393.4	17.8	4803	4	AAD11574 Human pho
38	393.4	17.5	4820	4	AA11388 Human pho
39	385.8	17.5	2547	6	ABA9497 Human lip
40	365	16.6	2694	6	ABL51366 Mouse pho
41	358.6	16.3	3112	6	ABL51352 Mouse pho
42	342.8	15.6	369	3	AAA44804 Human sec
43	336.2	15.3	2397	6	AA36905 Human pho
44	324	14.7	4875	4	AA11386 Human pho
45	321.4	14.6	1317	5	AA584338 DNA enco

ALIGNMENTS

RESULT 1
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ID AA53270 standard; cDNA; 2204 BP.
XX
AC AA53270;
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DT 05-OCT-2000 (first entry)
XX
DE Human phospholipase 2 HPPL2 coding sequence.
XX
KW Human; phospholipase 2; HPPL2; cancer; autoimmune disorder;
KW inflammatory disorder; reproductive disorder; infection; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 95..1912
FT /tag= a
FT /product= "HPPL2"
XX
PN WO200024911-A2.
XX
PD 04-MAY-2000.
XX
PF 27-OCT-1999; 99WO-US025021.
XX
PR 27-OCT-1998; 98US-00181317.
PR 21-JAN-1999; 99US-00234726.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Bardman O, Guegler KJ, Corley NC, Baughn MR,
PI Azimzai Y, Lal P, Lu DAM;
XX
DR WPI; 2000-350750/30.
XX
PT P-PSDB; AAB03628.
XX
PT Human phospholipase genes and proteins useful to diagnose, prevent or
PT treat cancer, autoimmune or inflammatory or reproductive disorders.
XX
PS Claim 9; Page 74-75; 80pp; English.
XX
CC The present sequence is the coding sequence of human phospholipase 2
CC (HPPL2). The protein produced from this sequence is involved in the
CC hydrolysis of membrane phospholipids. The protein and its coding sequence
CC can be used to diagnose and treat the following: cancers such as

CC prostate, breast and testicular cancers, autoimmune and inflammatory
 CC disorders such as AIDS, allergies, anaemia, asthma, atherosclerosis,
 CC Crohn's disease, diabetes mellitus, emphysema, Graves' disease, irritable
 CC bowel syndrome, multiple sclerosis, myasthenia gravis, psoriasis,
 CC rheumatoid arthritis and systemic lupus erythematosus, infection caused
 CC by viruses, fungi, bacteria, parasites and protozoa, and reproductive
 CC disorders including infertility, disruptions of the menstrual cycle,
 CC polycystic ovary syndrome, ectopic pregnancies, disruptions of
 CC spermatogenesis, cancers within the reproductive tract and impotence. The
 CC present sequence was obtained from clone no.1430683, which was
 CC constructed using ileum tissue
 XX
 SQ

Sequence 2204 BP; 429 A; 686 C; 625 G; 462 T; 0 U; 2 Other;

Query Match 99.9%; Score 2202; DB 3; Length 2204;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CATGGTTGGGGCGCAGAGGGCAGGNANACCAAGGGAGAGAGGGGAAATTGCGCC	60
DB	1	CATGGTTGGGGCGCAGAGGGCAGGNANACCAAGGGAGAGAGGGGAAATTGCGCC	60
QY	61	CTTTTGGGTGAAGCTGTTATGCTGAGCTTAATGATCTTCTGAGTGTGTCGCCAC	120
DB	61	CTTTTGGGTGAAGCTGTTATGCTGAGCTTAATGATCTTCTGAGTGTGTCGCCAC	120
QY	121	CTTGGCCCTCTGCTTTGAGAGAGTGGCTTCTACCTCACAGACACAGGATTTATGGTCT	180
DB	121	CTTGGCCCTCTGCTTTGAGAGAGTGGCTTCTACCTCACAGACACAGGATTTATGGTCT	180
QY	181	TTTCTGCCCGCCCTGCTGGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	240
DB	181	TTTCTGCCCGCCCTGCTGGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	240
QY	241	CCAGGCTGAGTGCAATGCGTGATCTGCTCAGCTGCAACCTCCGCTCTGGGTTCAA	300
DB	241	CCAGGCTGAGTGCAATGCGTGATCTTGGCTCAGTCAACCTCCGCTCTGGGTTCAA	300
QY	301	GGGATTCCTGCTCAGCTCCCGAGTAGCTGGGATTACAGACTGAGGAGCTGGCCGT	360
DB	301	GGGATTCCTGCTCAGCTCCCGAGTAGCTGGGATTACAGACTGAGGAGCTGGCCGT	360
QY	361	GGGATTCCTGCTCAGCTCCCGAGTAGCTGGGATTACAGACTGAGGAGCTGGCCGT	420
DB	361	GGGATTCCTGCTCAGCTCCCGAGTAGCTGGGATTACAGACTGAGGAGCTGGCCGT	420
QY	421	GGTGGCCGCGCTTGGAGCAGGCTGAGCTGGATGAGACCTGAGGAGGATGAGAT	480
DB	421	GGTGGCCGCGCTTGGAGCAGGCTGAGCTGGATGAGACCTGAGGAGGATGAGAT	480
QY	481	CCGAGTGTAGCTATTATGGCCACTGGTGGGATCCGGGCAATGACTTCCCTGTATGG	540
DB	481	CCGAGTGTAGCTATTATGGCCACTGGTGGGATCCGGGCAATGACTTCCCTGTATGG	540
QY	541	CGAGCTGGCTGCTGAGGAGCTGGGCTCTTGGATGCGTCTCTATCATCAGCGGGC	600
DB	541	CGAGCTGGCTGCTGAGGAGCTGGGCTCTTGGATGCGTCTCTATCATCAGCGGGC	600
QY	601	CTCGGGCTCCACTGGGCTTGGCCAACTTTATGAGGACCCAGAGTGGTCTCAGAAGGA	660
DB	601	CTCGGGCTCCACTGGGCTTGGCCAACTTTATGAGGACCCAGAGTGGTCTCAGAAGGA	660
QY	661	CTTGGAGGGCCCACTGAGTGTCTGAAGACCCAGGTGACCAAGTGGGTGTGCT	720
DB	661	CTTGGAGGGCCCACTGAGTGTCTGAAGACCCAGGTGACCAAGTGGGTGTGCT	720
QY	721	GSCCCCAAGCTGAGCGGTACCGCAGAGCTGGCCGAGCTGGCCGCTTGGGCTA	780
DB	721	GSCCCCAAGCTGAGCGGTACCGCAGAGCTGGCCGAGCTGGCCGCTTGGGCTA	780
QY	781	CCCAAGCTGCTTCAACCACTGTGGGCCCTCATCAACAGAGGCGTGTGATGATGAGCC	840
DB	781	CCCAAGCTGCTTCAACCACTGTGGGCCCTCATCAACAGAGGCGTGTGATGATGAGCC	840

QY	841	CCATGATCAAGCTCTCAGATCAACGGGAGGCGCTGAGTCAATGGCCAGAACCTCTGCCC	900
DB	841	CCATGATCAAGCTCTCAGATCAACGGGAGGCGCTGAGTCAATGGCCAGAACCTCTGCCC	900
QY	901	CATCTACTGTGCGCTCAACACCAAGGGAGAGCTGACCACTTTTGAATTTGGGGAGTG	960
DB	901	CATCTACTGTGCGCTCAACACCAAGGGAGAGCTGACCACTTTTGAATTTGGGGAGTG	960
QY	961	GTGCGAGTCTCTCCCTAAGAGTTCGGCTTCCCAAGTAGCGGGGCTTCAATCCCTCTGA	1020
DB	961	GTGCGAGTCTCTCCCTAAGAGTTCGGCTTCCCAAGTAGCGGGGCTTCAATCCCTCTGA	1020
QY	1021	GCTCTTTTGGCTCCGAGTCTTTTATGGGGAGCTGATGAAGAGGCTTCTGAGTCCGCGAT	1080
DB	1021	GCTCTTTTGGCTCCGAGTCTTTTATGGGGAGCTGATGAAGAGGCTTCTGAGTCCGCGAT	1080
QY	1081	CTGCTTCTTAGAAGGTATCTGAGCAACCTGTATGAGCAACCTCCAGACAGCTTATA	1140
DB	1081	CTGCTTCTTAGAAGGTATCTGAGCAACCTGTATGAGCAACCTCCAGACAGCTTATA	1140
QY	1141	CTGGGCTCAGAGCCAGCCAGTCTTGGGACCGCTGGGTCAAGAACAGGCCAACTCTGGA	1200
DB	1141	CTGGGCTCAGAGCCAGCCAGTCTTGGGACCGCTGGGTCAAGAACAGGCCAACTCTGGA	1200
QY	1201	CAAGGAGAGGTTCCCTTCTGAAGATAGAAGAACCACTTCAAGCCGCGGAGATAGC	1260
DB	1201	CAAGGAGAGGTTCCCTTCTGAAGATAGAAGAACCACTTCAAGCCGCGGAGATAGC	1260
QY	1261	TGAGTTTTTTCACCGATCTTCTGACGTTGGCTTCCACCTGGGCCAGGCCACATAATTTCT	1320
DB	1261	TGAGTTTTTTCACCGATCTTCTGACGTTGGCTTCCACCTGGGCCAGGCCACATAATTTCT	1320
QY	1321	GGTGGCTCCATTTTCCAAAGACTATCTTTTCAAGATCTCTTCCACATGGAAGC	1380
DB	1321	GGTGGCTCCATTTTCCAAAGACTATCTTTTCAAGATCTCTTCCACATGGAAGC	1380
QY	1381	TACCACTCTGGATGGCTCCCAACAGCTGACACCTCGAGGCCACCTGTCCTGCT	1440
DB	1381	TACCACTCTGGATGGCTCCCAACAGCTGACACCTCGAGGCCACCTGTCCTGCT	1440
QY	1441	GGATGTGGCTACCTCATCAATACAGCTGCTTCCCTTCTGCAAGCCACTCGGAGCT	1500
DB	1441	GGATGTGGCTACCTCATCAATACAGCTGCTTCCCTTCTGCAAGCCACTCGGAGCT	1500
QY	1501	GGACCTCATCTCTGATTTGGACTACAACTCCACGAGCTTCCAGCAGTTCAGCTCT	1560
DB	1501	GGACCTCATCTCTGATTTGGACTACAACTCCACGAGCTTCCAGCAGTTCAGCTCT	1560
QY	1561	GGGCGGCTTCTGCGAGGAGCGGGATCCCGTTCCACCCATCTCGCCAGCCCGAAGA	1620
DB	1561	GGGCGGCTTCTGCGAGGAGCGGGATCCCGTTCCACCCATCTCGCCAGCCCGAAGA	1620
QY	1621	GGAGCTCCAGCTCCGGAGTGCCACACTTTCGACCCCTTCCGCGGAGCCCTGCG	1680
DB	1621	GGAGCTCCAGCTCCGGAGTGCCACACTTTCGACCCCTTCCGCGGAGCCCTGCG	1680
QY	1681	GGTGTGACATTTTCTCTGGGTCGGGGGACACCGGAGGCGGAGCTGGGGAGGT	1740
DB	1681	GGTGTGACATTTTCTCTGGGTCGGGGGACACCGGAGGCGGAGCTGGGGAGGT	1740
QY	1741	GAACTGTCTTCTCATCGGACTCTCCCTACACTACACGAAGGTGACTACAGCAGGAGA	1800
DB	1741	GAACTGTCTTCTCATCGGACTCTCCCTACACTACACGAAGGTGACTACAGCAGGAGA	1800
QY	1801	CGTGCAAGAGCTGTCGACCTGACATTAATGTCTGCAACAACTAGGAGCAGTGT	1860
DB	1801	CGTGCAAGAGCTGTCGACCTGACATTAATGTCTGCAACAACTAGGAGCAGTGT	1860
QY	1861	GGAGCTCTGCGCAGGAGTGACGAGGCGGAGCGGAGCCCGCTGATGCGCGG	1920
DB	1861	GGAGCTCTGCGCAGGAGTGACGAGGCGGAGCGGAGCCCGCTGATGCGCGG	1920

QY 1921 GCCCTGCCACCCCTAACTCTCATTTCCCTGGCTGCTGAGTTCAGGTGGAACTGT 1980
 Db 1921 GCCCTGCCACCCCTAACTCTCATTTCCCTGGCTGCTGAGTTCAGGTGGAACTGT 1980
 QY 1981 CATCAGCAGTGTTCAGAGCCTCGGCTCAGTGGCACTGTCACAGGTTCAGGTGAG 2040
 Db 1981 CATCAGCAGTGTTCAGAGCCTCGGCTCAGTGGCACTGTCACAGGTTCAGGTGAG 2040
 QY 2041 GGTGGAGTCCCTTGGCCCTCAGCAGTTTGCAGTGGGTAAAGAGGCCAAGCCCATTT 2100
 Db 2041 GGTGGAGTCCCTTGGCCCTCAGCAGTTTGCAGTGGGTAAAGAGGCCAAGCCCATTT 2100
 QY 2101 GTGTAATACCCAAACCCCGCCCTGTGCTGTTTCCCTTCTGCGTACCTTGAGTA 2160
 Db 2101 GTGTAATACCCAAACCCCGCCCTGTGCTGTTTCCCTTCTGCGTACCTTGAGTA 2160
 QY 2161 GTTGGAGCACTTGATACATCAGACCTCATACAAAATAAAAAA 2204
 Db 2161 GTTGGAGCACTTGATACATCAGACCTCATACAAAATAAAAAA 2204

RESULT 2

AAZ88757
 ID AAZ88757 standard; cDNA; 3085 BP.
 AC AAZ88757;
 XX 18-MAY-2000 (first entry)
 DT 18-MAY-2000 (first entry)
 XX Human PLA2 cDNA.
 DE PLA2; phospholipase A2; phosphatide 2-acyl hydrolase; human; therapy;
 KW arachidonic acid; lysophospholipid; Alzheimer's disease; ss.
 XX Homo sapiens.

OS Key Location/Qualifiers
 XX 48..2789
 FH CDS
 FT /*tag= a
 FT /product= "PLA2"

PN US6025178-A.

PD 15-FEB-2000.

PF 28-MAR-1997; 97US-00827208.

PR 29-MAR-1996; 96US-0014608P.

PS (ELIL) LILLY & CO ELI.

PI Sharp JD, Strifler BA, Choiu XC, Kramer RM, Pickard RT;

XX WPI; 2000-181816/16.

DR P-PSDB; AAY51557.

PT An isolated amino acid having phospholipase (PL)A2 activity is useful in
 PT assays to identify inhibitors having a therapeutic benefit, such as
 PT inhibiting the central role of PLA2 in the inflammatory component of
 PT Alzheimer's disease.

PS Example 5; Col 47-54; 32pp; English.

XX This invention describes a novel human phospholipase A2 (PLA2) protein
 CC (I) and its encoding nucleic acid. The amino acid (I) releases
 CC arachidonic acid in specific tissues characterized by unique membrane
 CC phospholipids, by generating lysophospholipid species which are
 CC deleterious to membrane integrity or by remodeling of unsaturated species
 CC of membrane phospholipids through deacylation/reacylation mechanisms. The
 CC amino acid is useful in assays to identify inhibitors having a
 CC therapeutic benefit, such as inhibiting the central role of PLA2 in the
 CC inflammatory component of Alzheimer's disease. The amino acid (I) allows
 CC sensitive and rapid screening and identification of inhibitors of

CC phospholipase A2. This sequence encodes the human PLA2 protein (also
 CC known as phosphatide 2-acyl hydrolase)
 XX Sequence 3085 BP; 607 A; 959 C; 907 G; 612 T; 0 U; 0 Other;
 SQ
 Query Match 82.4%; Score 1816.8; DB 3; Length 3085;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 1861; Conservative 0; Mismatches 2; Indels 33; Gaps 1;
 QY 342 GACTGAGGAGTGGCCGTGCGACTGGCTTCGGGCCCTTGCGAGGAGCAGCCCTTCC 401
 Db 1186 GACTGAGGAGTGGCCGTGCGACTGGCTTCGGGCCCTTGCGAGGAGCAGCCCTTCC 1245
 QY 402 TGAGCAGGAGGAAGCAGGTGGTGGGCCCTTGAGGAGGCCCTTGAGTGGATGAG 461
 Db 1246 TGAGCAGGAGGAAGCAGGTGGTGGGCCCTTGAGGAGGCCCTTGAGTGGATGAG 1305
 QY 462 ACCTGAGGAGGATGAGATCCCGAGTGGTAGCTATTATGSCCACTGGTGGTGGATCCGG 521
 Db 1306 ACCTGAGGAGGATGAGATCCCGAGTGGTAGCTATTATGSCCACTGGTGGTGGATCCGG 1365
 QY 522 CAATGACTTCCCTGTATGGGAGCTGGCTGAGGAGCTGGGCCCTTCTTGGATGG 581
 Db 1366 CAATGACTTCCCTGTATGGGAGCTGGCTGAGGAGCTGGGCCCTTCTTGGATGG 1425
 QY 582 TCTCCTACATCACCGGGGCTGGGCTCCACTGGGCCCTTGCCCAACCTTTATGAGGACC 641
 Db 1426 TCTCCTACATCACCGGGGCTGGGCTCCACTGGGCCCTTGCCCAACCTTTATGAGGACC 1485
 QY 642 CAGAGTGGTCTCAGAAAGACCTGGCAGGGCCACTGAGTTGCTGAAGACCCAGGTGACCA 701
 Db 1486 CAGAGTGGTCTCAGAAAGACCTGGCAGGGCCACTGAGTTGCTGAAGACCCAGGTGACCA 1545
 QY 702 AGAACAGCTGGGTGTGCTGGCCCCCAGCCAGCTGACGGGTACCGGAGGAGCTGGCCG 761
 Db 1546 AGAACAGCTGGGTGTGCTGGCCCCCAGCCAGCTGACGGGTACCGGAGGAGCTGGCCG 1605
 QY 762 AGCGTGCCCGCTTGGGCTACCCAGCTGCTTCCAGAACCTTGGGCCCTTCATCAACGAGG 821
 Db 1606 AGCGTGCCCGCTTGGGCTACCCAGCTGCTTCCAGAACCTTGGGCCCTTCATCAACGAGG 1665
 QY 822 CGCTGCTGCATGATGAGCCCCCATGATCAACAGCTCTCAGATCAACGGGAGGCCCTGAGTC 881
 Db 1666 CGCTGCTGCATGATGAGCCCCCATGATCAACAGCTCTCAGATCAACGGGAGGCCCTGAGTC 1725
 QY 882 ATGCCAGAACCTCTGCCCCATCTACTGTGCCCTCAACACCAAGGGCAGAGCCTGACCA 941
 Db 1726 ATGCCAGAACCTCTGCCCCATCTACTGTGCCCTCAACACCAAGGGCAGAGCCTGACCA 1785
 QY 942 CTTTGAATTTGGGAGTGGTGGAGTTCCTCCCTACGAGGTGGCTTCCCAAGTACG 1001
 Db 1786 CTTTGAATTTGGGAGTGGTGGAGTTCCTCCCTACGAGGTGGCTTCCCAAGTACG 1845
 QY 1002 GGGCCTTCATCCCTCTGAGCTCTTTGGCTCCGAGTTCCTTATGGGCGAGCTGATGAGA 1061
 Db 1846 GGGCCTTCATCCCTCTGAGCTCTTTGGCTCCGAGTTCCTTATGGGCGAGCTGATGAGA 1905
 QY 1062 GGGTCTCTGAGTCCCGCATCTGCTTTTGAAGGTATCTGGAGCAACCTGTATGACGCA 1121
 Db 1906 GGGTCTCTGAGTCCCGCATCTGCTTTTGAAGGTATCTGGAGCAACCTGTATGACGCA 1965
 QY 1122 ACCTCCAGGACAGCTTATCTGGGCCCTCAGAGCCAGCCAGTCTTGGGACCGCTGGGTCA 1181
 Db 1966 ACCTCCAGGACAGCTTATCTGGGCCCTCAGAGCCAGCCAGTCTTGGGACCGCTGGGTCA 2025
 QY 1182 GGAACCCAGGCCAACCCTGGCAAGAGCAGTCCCGCTTCTGAAGATAGAGAACCCCT 1241
 Db 2026 GGAACCCAGGCCAACCCTGGCAAGAGCAGTCCCGCTTCTGAAGATAGAGAACCCCT 2085
 QY 1242 CAACGCCCGCAGAAATGCTGAGTTTTTCAACCGATCTTCTGACGTGGCGTCCACTGGCCC 1301
 Db 2086 CAACGCCCGCAGAAATGCTGAGTTTTTCAACCGATCTTCTGACGTGGCGTCCACTGGCCC 2145

described are: (1) an isolated polynucleotide (II) comprising an 8517 base pair sequence, given in AAF7498; (2) an expression vector (III) comprising (I) and an expression control sequence; (3) a host cell transformed with (III); (4) an expression vector (IV) comprising (II) operably linked to an expression control sequence; and (5) a host cell transformed with (IV). (I) is useful for screening compounds which inhibit or block cytosolic PLA2 (cPLA2) enzyme activity. The host cells transformed or transfected with cPLA2 enzymes in large quantities which are useful in screening assays for discovering agents that inhibit PLA2. The inhibitors identified are useful for treating inflammatory conditions such as rheumatoid arthritis, psoriasis, or asthma. (I) is also useful in the detection of mutant genomic DNA which has been digested with restriction enzymes and run on an electrophoretic gel by hybridising to the genomic DNA.

Sequence 3085 BP: 607 A; 859 C; 907 G; 612 T; 0 U; 0 Other; XX
Sequence 3085 BP: 607 A; 859 C; 907 G; 612 T; 0 U; 0 Other; SO

Query Match

Query Macchi	Best Local Similarity	82.4%	pred. No. 0:	score 1813.8
			98.2%	

BEST LOCAL SIMILARITY	98.2%	FREQ. NO.: 0;
Matches 1861:	Conservative	0: Mismatches
		2; Indels
		33; Gaps

Qy	342	GA	CTGAGGGAGCTGGCGCTGGCTGGACTGGGCTTCGGGCGCTTGGCAGAGGACGAGCGCTTCC	401
Db	1186	GA	CTGAGGAGCTGGCGCTGGCTGGACTGGGCTTCGGGCGCTTGGCAGAGGACGAGCGCTTCC	1245
Qy	402	TG	ACACGAGGAGACGAGCTGGTGGCGCGCGCTTTGAGGCAGGCGCCCTGACGCTGGATGAG	461
Db	1246	TG	ACACGAGGAGGACGAGCTGGTGGCGCGCGCTTTGAGGCAGGCGCCCTGACGCTGGATGAG	1305
Qy	462	AC	CTGACGAGGAGATGAGATCCCACTGGTAGCTATTATGGCCACTCTGGTGGGATCCGGG	521
Db	1306	AC	CTGACGAGGAGATGAGATCCCACTGGTAGCTATTATGGCCACTCTGGTGGGATCCGGG	1365
Qy	522	CA	ATGACTTCCCTGTATGGGAGCTGGCTGGCGCTGAAGGAGCTGGGCGCTTGGATTGGG	581
Db	1366	CA	ATGACTTCCCTGTATGGGAGCTGGCTGGCGCTGAAGGAGCTGGGCGCTTGGATTGGG	1425
Qy	582	TCT	CCTACATCACGGGGCTCGGGCTCCACCTGGGCGCTTGGCGCAACCTTTATGAGGACC	641
Db	1426	TCT	CCTACATCACGGGGCTCGGGCTCCACCTGGGCGCTTGGCGCAACCTTTATGAGGACC	1485
Qy	642	CAG	AGTGGTCTCACAAGGACCTGGCAGGGGCCACTGAGTTGCTGAAAGACCCAGGTGACCA	701
Db	1486	CAG	AGTGGTCTCACAAGGACCTGGCAGGGGCCACTGAGTTGCTGAAAGACCCAGGTGACCA	1545
Qy	702	AGA	ACAAGCTGGGTGTGTGGCCCCCAGCAGCTGACGGGTACCGGCGAGGAGCTGGCGG	761
Db	1546	AGA	ACAAGCTGGGTGTGTGGCCCCCAGCAGCTGACGGGTACCGGCGAGGAGCTGGCGG	1605
Qy	762	AG	CTGCCCGCTTGGGCTACCAAGCTGCTTACCACCTGTGGCGCTCATCAACGAGG	821
Db	1606	AG	CTGCCCGCTTGGGCTACCAAGCTGCTTACCACCTGTGGCGCTCATCAACGAGG	1665
Qy	822	CG	TGCTCATGATCAGCCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCGCTTGAGTC	881
Db	1666	CG	TGCTCATGATGAGCCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCGCTTGAGTC	1725
Qy	882	AT	GCCAGAACCCCTCTGCCCATCTACTGTGCCCTCAACACAAAGGGCGAGCGCTGACCA	941
Db	1726	AT	GCCAGAACCCCTCTGCCCATCTACTGTGCCCTCAACACAAAGGGCGAGCGCTGACCA	1785
Qy	942	CT	TTTGAATTTGGGAGTGGTGGGAGTTCTCTCCCTACGAGTGGGCTTCCCAAGTACG	1001
Db	1786	CT	TTTGAATTTGGGAGTGGTGGGAGTTCTCTCCCTACGAGTGGGCTTCCCAAGTACG	1845
Qy	1002	GG	CGCTTCAATCCCTCTCAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA	1061
Db	1846	GG	CGCTTCAATCCCTCTCAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA	1905
Qy	1062	GG	CTTCTCAGTCCGCACTCTGCTTCTTTAGAAGGTATCTGGAGCAACTGTATGACGCCA	1121
Db	1906	GG	CTTCTCAGTCCGCACTCTGCTTCTTTAGAAGGTATCTGGAGCAACTGTATGACGCCA	1965

Db	2746	UGCGCCAGGACAGUGAGCGGAGCGGCGGACGCGAGGCCCCACUGAUGGCGGGGCCCCUGC	2805
QY	1929	CACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTTCAGAGTGGGACTGTCTATCAGC	1988
Db	2806	CACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTTCAGAGTGGGACTGTCTATCAGC	2865
QY	1989	AGTGCTTCAGAGCCTCGGGCTCAGTGTGCATGTGCCAGGTCCAGGCTGAGGGCTCGGA	2048
Db	2866	AGTGCTTCAGAGCCTCGGGCTCAGTGTGCATGTGCCAGGTCCAGGCTGAGGGCTCGGA	2925
QY	2049	GTCCTCTTGCGCTCAGCAGTTTCAGTGGGGTAAGGAGGCCAAGCCATTTGTGTAATC	2108
Db	2926	GCUCCTUUGGCGCCUCAGCAGUUUGCAGUGGGGUAAGAGGCCAAGCCAUUUGUGUAUC	2985
QY	2109	ACCCAAAAACCCCGGCTGTGCTGTTTTCCTTCTGCGGTACCTTGAGTGTGGAGC	2168
Db	2986	ACCCAAAAACCCCGGCTGTGCTGTTTTCCTTCTGCGGTACCTTGAGTGTGGAGC	3045
QY	2169	ACTTGATCATCTACAGACTCATACAAAAAATAAAAA	2204
Db	3046	ACUUGAUAUCAACAGACAGUCUAUACAAAAAATAAAAA	3081

expression vector con

expression vector con

CC	PLA2, contacting it with a candidate compound, and determining whether									
CC	the PLA2 activity has been inhibited. The assay provides rapid and									
CC	efficient screening for new antiinflammatory drugs that inhibit the									
CC	arachidonic acid cascade. These may be especially useful in the treatment									
CC	of the inflammatory component of Alzheimer's disease									
XX										
SQ	Sequence 3085 BP; 607 A; 959 C; 907 G; 612 T; 0 U; 0 Other;									
	Query Match	82.4%;	Score	1816.8;	DB	4;	Length	3085;		
	Best local Similarity	98.2%;	Pred. No.	0;						
	Matches 1861;	Conservative	0;	Mismatches	2;	Indels	33;	Gaps	1;	
QY	342	GACTGAGGAGCTGGCGCTGCGAGTGGGCTTCGGGCTTCGGGCTTCGAGAGGACGAGCTTCC	401							
DB	1186	GACTGAGGAGCTGGCGCTGCGAGTGGGCTTCGGGCTTCGGGCTTCGAGAGGACGAGCTTCC	1245							
QY	402	TGAGCAGGAGGAGGAGCTGGCTGCGCGCGGCTTTGAGCGAGGCGCTTCGAGCTGGATGGAG	461							
DB	1246	TGAGCAGGAGGAGGAGCTGGCTGCGCGCGGCTTTGAGCGAGGCGCTTCGAGCTGGATGGAG	1305							
QY	462	ACCTGCAGGAGGATGAGATCCCAAGTGTAGTATATATGGCCACTGTGGTGGATCCGGG	521							
DB	1306	ACCTGCAGGAGGATGAGATCCCAAGTGTAGTATATATGGCCACTGTGGTGGATCCGGG	1365							
QY	522	CAATGACTTCCCTGATGGGAGCTGGCTGGCTGAGGAGCTGGGCTCTTTGATTTGCG	581							
DB	1366	CAATGACTTCCCTGATGGGAGCTGGCTGGCTGAGGAGCTGGGCTCTTTGATTTGCG	1425							
QY	582	TCTCTCATACACCGGGCTTCGGGCTCCACTTCGGGCTTCGGCCAACTTTATGAGACC	641							
DB	1426	TCTCTCATACACCGGGCTTCGGGCTCCACTTCGGGCTTCGGCCAACTTTATGAGACC	1485							
QY	642	CAGAGTGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTCGTAAGACCCAGGTGACCA	701							
DB	1486	CAGAGTGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTCGTAAGACCCAGGTGACCA	1545							
QY	702	AGAACAGCTGGGTGTGTCGCCCCCAGCCAGCTGACGGGTACCGGAGAGCTGGCGG	761							
DB	1546	AGAACAGCTGGGTGTGTCGCCCCCAGCCAGCTGACGGGTACCGGAGAGCTGGCGG	1605							
QY	762	AGCGTGCCGCTTGGGCTTACCAGCTGCTTACCAGCTGCTGGGCCCTCATCAACGAGG	821							
DB	1606	AGCGTGCCGCTTGGGCTTACCAGCTGCTTACCAGCTGCTGGGCCCTCATCAACGAGG	1665							
QY	822	CGCTGCTGCATGATGAGCCCCATGATCAAGCTCTCAGATCAACGGGAGGCGCTGAGTC	881							
DB	1666	CGCTGCTGCATGATGAGCCCCATGATCAAGCTCTCAGATCAACGGGAGGCGCTGAGTC	1725							
QY	882	ATGGCCAGAACCTCTGCCCATCTACTGTGCCCTCAACACCAAGGGCAGAGCTGACCA	941							
DB	1726	ATGGCCAGAACCTCTGCCCATCTACTGTGCCCTCAACACCAAGGGCAGAGCTGACCA	1785							
QY	942	CTTTTGAATTTGGGAGTGGTGGAGTTCTCTCCCTACGAGGTTCGGCTTCCCAAGTAGC	1001							
DB	1786	CTTTTGAATTTGGGAGTGGTGGAGTTCTCTCCCTACGAGGTTCGGCTTCCCAAGTAGC	1845							
QY	1002	GGGCTTCTATCCCTCTGAGCTTTTGGCTCCGAGTTCTTTATGGGCGAGCTGATCAAGA	1061							
DB	1846	GGGCTTCTATCCCTCTGAGCTTTTGGCTCCGAGTTCTTTATGGGCGAGCTGATCAAGA	1905							
QY	1062	GGCTTCTGAGTCCCGCATCTGCTTCTAGAAGTATCTGAGCAACCTGTATGACGCCA	1121							
DB	1906	GGCTTCTGAGTCCCGCATCTGCTTCTAGAAGTATCTGAGCAACCTGTATGACGCCA	1181							
QY	1122	ACCTCCAGGACAGCTTATCTGGGCTTCAGAGCCAGCCAGTTCGGGACCGCTGGGTCA	1181							
DB	1966	ACCTCCAGGACAGCTTATCTGGGCTTCAGAGCCAGCCAGTTCGGGACCGCTGGGTCA	2025							
QY	1182	GGAAACAGGACCACTGGAACAAGGAGAGTTCCTCCCTTCTGAAGATAGAAGAACCCCT	1241							
DB	2026	GGAAACAGGACCACTGGAACAAGGAGAGTTCCTCCCTTCTGAAGATAGAAGAACCCCT	2085							
QY	1242	CAACAGCGCGCAGAATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCATGGGCC	1301							

RESULT 8
AAS17363
ID AAS17363 standard; cDNA; 2699 BP.
XX
AC AAS17363;

DB	2086	CAACAGCGCGCAGAAATAGCTGAGTTTTCACCGATCTTCTGACGTGGGCTCCACTGGGCC	2145							
QY	1302	AGGCCACACATAAATTTCTGCGCTGGCCTCAATTTCCAAAAGACTACTTTGACGATCCTC	1361							
DB	2146	AGGCCACACATAAATTTCTGCGCTGGCCTCAATTTCCAAAAGACTACTTTGACGATCCTC	2205							
QY	1362	ACTTCTCCACATGGAAGCTACACTCTGGATGGGCTCCCAACAGCTGACACCCCTCGG	1421							
DB	2206	ACTTCTCCACATGGAAGCTACACTCTGGATGGGCTCCCAACAGCTGACACCCCTCGG	2265							
QY	1422	AGCCCCACCTGTGCGCTGGATTTGGCTACTCATCAATACCACTGCTGCCCTCTC	1481							
DB	2266	AGCCCCACCTGTGCGCTGGATTTGGCTACTCATCAATACCACTGCTGCCCTCTC	2325							
QY	1482	TGACAGCCCACTCGGGAGCTGGACCTCATCTGTCAATGGACTCAACCTCCAGGACCT	1541							
DB	2326	TGACAGCCCACTCGGGAGCTGGACCTCATCTGTCAATGGACTCAACCTCCAGGACCT	2385							
QY	1542	TCACAGAGTTGAGCTCTCGGGCGGTTCTGCCAGGAGCAGGGATCCCGTTCCCAACCA	1601							
DB	2386	TCACAGAGTTGAGCTCTCGGGCGGTTCTGCCAGGAGCAGGGATCCCGTTCCCAACCA	2445							
QY	1602	TCTCGCCAGCCCGAAGAGCAGCTCCAGCTCGGGAGTGCCACACCTTCTCCAGCCCA	1661							
DB	2446	TCTCGCCAGCCCGAAGAGCAGCTCCAGCTCGGGAGTGCCACACCTTCTCCAGCCCA	2505							
QY	1662	CCTGCCCCGGAGCCCTTCGGTGTCTGCACTTTT	1693							
DB	2506	CCTGCCCCGGAGCCCTTCGGTGTCTGCACTTTTCTGCTCAGCGACTCTCTCCGGGAGT	2565							
QY	1694	-----TCTCTGCGGTTCGGGCGGACACCCGAGGAGGCGGAGCTGGGAGGTGAACCTGT	1748							
DB	2566	ACTCGGCCCTTCGGGCTTCGGCGGACACCCGAGGAGGCGGAGCTGGGAGGTGAACCTGT	2625							
QY	1749	CTTCATCGGACTCTCCCTTACCCTACACGAAGGTGACCTACAGCCAGAGGACGTGGACA	1808							
DB	2626	CTTCATCGGACTCTCCCTTACCCTACACGAAGGTGACCTACAGCCAGAGGACGTGGACA	2685							
QY	1809	AGCTGCTGCACCTGACACATTAATGCTGCAACACAGAGCAGCTGTGGAGGCTC	1868							
DB	2686	AGCTGCTGCACCTGACACATTAATGCTGCAACACAGAGCAGCTGTGGAGGCTC	2745							
QY	1869	TGCGCCAGGAGTGAGCGGAGGCGGAGCGGCGGAGCTGATGGCGGGGCGGCTGTC	1928							
DB	2746	TGCGCCAGGAGTGAGCGGAGGCGGAGCGGCGGAGCTGATGGCGGGGCGGCTGTC	2805							
QY	1929	CACCCCTAACTCTCATTCCTTCCCTGGCTGTGAGTTGAGGTGGGAACTGTCAACGC	1988							
DB	2806	CACCCCTAACTCTCATTCCTTCCCTGGCTGTGAGTTGAGGTGGGAACTGTCAACGC	2865							
QY	1989	AGTGTCTCAGAGCTCGGCTCAGGTGGCACTGTCCAGGTTCCAGGCTGAGGCTGGGA	2048							
DB	2866	AGTGTCTCAGAGCTCGGCTCAGGTGGCACTGTCCAGGTTCCAGGCTGAGGCTGGGA	2925							
QY	2049	GTCCTCTCGGCTCAGCAGTTTTCAGTGGGTTAAGGAGGCCAAGCCATTTGTGTAATC	2108							
DB	2926	GTCCTCTCGGCTCAGCAGTTTTCAGTGGGTTAAGGAGGCCAAGCCATTTGTGTAATC	2985							
QY	2109	ACCCAAACCCCGGCTGTGCTTTTCCCTTCTGCGCTACCTGTAGTAGTTGGAGC	2168							
DB	2986	ACCCAAACCCCGGCTGTGCTTTTCCCTTCTGCGCTACCTGTAGTAGTTGGAGC	3045							
QY	2169	ACTTGTATACATCAGACTCATCAAAAAA	2204							
DB	3046	ACTTGTATACATCAGACTCATCAAAAAA	3081							

Db	1529	GGCTTCTTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGAGCAAACTGTATGACGCA	1588
QY	1122	ACCTCCAGGACAGCTTATATCTGGGCTCAGAGCCCGACGCTCTGGAGCGGTGGGTCA	1181
Db	1589	ACCTCCAGGACAGCTTATCTGGGCTCAGAGCCCGACGCTCTGGAGCGGTGGGTCA	1648
QY	1182	GGAACTAGGCCAACTGGACAAAGGACAGGTCCCTCTTGAAGATAGAAGAACACCT	1241
Db	1649	GGAACTAGGCCAACTGGACAAAGGACAGGTCCCTCTTGAAGATAGAAGAACACCT	1708
QY	1242	CAACAGCCGGCAGATAGCTGAGTTTTCACCGATCTTCTGACGTGGGTGCCACTGGCC	1301
Db	1709	CAACAGCCGGCAGATAGCTGAGTTTTCACCGATCTTCTGACGTGGGTGCCACTGGCC	1768
QY	1302	AGCCACACATAATTTCTGCGTGGCTCCCATTTTCCAAAGACTACTTTTCAGCATCTC	1361
Db	1769	AGCCACACATAATTTCTGCGTGGCTCCCATTTTCCAAAGACTACTTTTCAGCATCTC	1828
QY	1362	ACTTCTCCACATGGAAGCTACCACTGGATGGCTCCCCAACCACTGACACCTCGG	1421
Db	1829	ACTTCTCCACATGGAAGCTACCACTGGATGGCTCCCCAACCACTGACACCTCGG	1888
QY	1422	AGCCCCACTCTGCTGGATGTTGGCTACCTCATCAATACAGCTGCTGCCCTCC	1481
Db	1889	AGCCCCACTCTGCTGGATGTTGGCTACCTCATCAATACAGCTGCTGCCCTCC	1948
QY	1482	TGCAGCCCACTCGGAGCGTGACCTCATCTGTCTATTGGACTACAACTCCACGGAGCT	1541
Db	1949	TGCAGCCCACTCGGAGCGTGACCTCATCTGTCTATTGGACTACAACTCCACGGAGCT	2008
QY	1542	TCCAGCAGTTGACGCTCTGGGCGGTTCTGCCAGGACGAGGGATCCGTTCCACCCA	1601
Db	2009	TCCAGCAGTTGACGCTCTGGGCGGTTCTGCCAGGACGAGGGATCCGTTCCACCCA	2068
QY	1602	TCTCGCCAGCCCGAGAGCAGCTCCAGCCTCGGAGTGCACACTTCTCGACCCCA	1661
Db	2069	TCTCGCCAGCCCGAGAGCAGCTCCAGCCTCGGAGTGCACACTTCTCGACCCCA	2128
QY	1662	CTTGCCCCGGAGCCCTGCGGTGTCACATTT-----	1693
Db	2129	CTTGCCCCGGAGCCCTGCGGTGTCACATTTCTCTGTGTACGCACTCCTTCCGGAGT	2188
QY	1694	-----TCTCTGGGTCCCGCGACACCCGAGAGCGGCAGCTGGGGAGGTGAACCTGT	1748
Db	2189	ACTCGGCCCCCTGGGTCCCGCGACACCCGAGAGCGGCAGCTGGGGAGGTGAACCTGT	2248
QY	1749	CTTCATCGGACTCTCCCTACCACTACAGAGGTGACCTACAGCCAGGAGGACGTGGACA	1808
Db	2249	CTTCATCGGACTCTCCCTACCACTACAGAGGTGACCTACAGCCAGGAGGACGTGGACA	2308
QY	1809	AGTGTGTCACTTGACACATTACAAATGTCTGCAACCAACAGAGCAGAGCTGCTGGAGGCTC	1868
Db	2309	AGTGTGTCACTTGACACATTACAAATGTCTGCAACCAACAGAGCAGAGCTGCTGGAGGCTC	2368
QY	1869	TGCGCCAGGAGTGCAGCGAGCGGCAGCGAGCCCACTGATGCGCGGGCCCCCTGC	1928
Db	2369	TGCGCCAGGAGTGCAGCGAGCGGCAGCGAGCCCACTGATGCGCGGGCCCCCTGC	2428
QY	1929	CACCCCTAACTCTCATTTCAATTCCTGGCTGCTGAGTTGAGGTGGAACTGTCTACGCG	1988
Db	2429	CACCCCTAACTCTCTCATTTCAATTCCTGGCTGCTGAGTTGAGGTGGAACTGTCTACGCG	2488
QY	1989	AGTGTCTCAGAGCCTCGGCTCAGGTGGCACTGTCACAGGTCACGCTGAGGCTGGGA	2048
Db	2489	AGTGTCTCAGAGCCTCGGCTCAGGTGGCACTGTCACAGGTCACGCTGAGGCTGGGA	2548
QY	2049	GTCCTCTGGCTCAGCAGTTTGACATGGGGTAAGAGGCGCAAGCCCACTTGTGTAATC	2108
Db	2549	GTCCTCTGGCTCAGCAGTTTGACATGGGGTAAGAGGCGCAAGCCCACTTGTGTAATC	2608
QY	2109	ACCCAAAACCCCGGCTGTGCTGTTTTTCCCTTCTCGCTACTCCTGAGTAGTGGAGC	2168

Db 2609 ACCAAAAACCCCGGCTGCTGCTGTTTCCCTTCTGCGCTACCTTGAGTAGTTGGAGC 2666

QY 2169 ACTTGATACATCACAGACTCATACAAA 2195
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Db 2669 ACTTGATACATCACAGACTCATACAAA 2695
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RESULT 10

AA517362

ID AAS17362 standard; cDNA; 4183 BP.

XX

AC AAS17362;

XX

DT 25-FEB-2002 (first entry)

XX

DE Partial cDNA encoding human cPLA2-beta enzyme.

XX

KW Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta;

KW U937 cell; membrane phospholipid turnover; intracellular signalling;

KW arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis;

KW psoriasis; asthma; inflammatory bowel disease; antiinflammatory; ss.

XX

OS Homo sapiens.

XX

FH Key

FT CDS

FT 1560..3896

FT /*tag= a

FT /partial

FT /product= "cPLA2-beta enzyme"

FT /note= "This sequence lacks a start codon"

XX

PN US6287838-B1.

XX

PD 11-SEP-2001.

XX

PF 13-DEC-1999; 99US-00460145.

XX

PR 24-JAN-1997; 97US-00788975.

XX

PA (GEMV) GENETICS INST INC.

XX

PI Kriz R, Song C;

XX

XX WPI; 2002-054342/07.

DR P-PSDB; AAU10696.

XX

PT Novel cytosolic phospholipase A2-beta enzyme encoding polynucleotide,

PT useful for producing the enzyme for use in assays to discover enzyme

PT antagonists.

XX

XX Claim 1; Col 11-15; 19pp; English.

XX

CC The present invention relates to a novel calcium-independent cytosolic

CC phospholipase A2 (cPLA2)-beta enzyme and the cDNA sequence encoding it.

CC The cDNA clone is isolated from U937 cells. The cPLA2 enzyme is active in

CC membrane phospholipid turnover and in regulation of intracellular

CC signalling mediated by the arachidonic acid cascade. The invention

CC describes a method for producing phospholipase enzymes which can be used

CC to identify inhibitors of their function. The inhibitors can be used

CC treat inflammatory disorders such as rheumatoid arthritis, psoriasis,

CC asthma, and inflammatory bowel disease. The present sequence represents a

CC partial cDNA sequence which encodes for human cPLA2-beta enzyme

XX

SQ Sequence 4183 BP; 983 A; 1177 C; 1168 G; 850 T; 0 U; 5 Other;

Query Match 82.0%; Score 1806.2; DB 6; Length 4183;

Best Local Similarity 98.1%; Pred. No. 0;

Matches 1851; Conservative 0; Mismatches 3; Indels 33; Gaps 1;

QY 342 GACTGAGGAGCTGGCCCTGCGACTGGGCTTCGGGCCCTGTGCAGAGCAGGCGCTTCC 401
 |||||

Db 2293 GACTGAGGAGCTGGCCCTGCGACTGGGCTTCGGGCCCTGTGCAGAGCAGGCGCTTCC 2352

QY	402	TGACGAGGAGGAGCAGGTGGTGGCCGCGGCTTTGAGGCGAGGCCCTGACGTGGATGGAG	461
Db	2353	TGACGAGGAGGAGCAGGTGGTGGCCGCGGCGCTTGAGGCGAGGCCCTGACGTGGATGGAG	2412
QY	462	ACCTGCAGAGGATGAGATCCACAGTGGTAGCTATTATGSGCCACATCTGGTGGATCCGGG	521
Db	2413	ACCTGCAGAGGATGAGATCCACAGTGGTAGCTATTATGSGCCACATCTGGTGGATCCGGG	2472
QY	522	CAATGACTTCCCTGTATGGCGACGTGGCTGGCCCTGAAGGAGCTGGGCTCTTTGATTTGG	581
Db	2473	CAATGACTTCCCTGTATGGCGACGTGGCTGGCCCTGAAGGAGCTGGGCTCTTTGATTTGG	2532
QY	582	TCTCTCAATCAACCGGGGCTTGGGGCTCCACTTGGGCTTGGCCCAACCTTTATCAGGACC	641
Db	2533	TCTCTCAATCAACCGGGGCTTGGGGCTCCACTTGGGCTTGGCCCAACCTTTATCAGGACC	2592
QY	642	CAGAGTGGTCTCAGAAAGGACCTGCGAGGCGCCACATGAGTTGCTGAAGACCCAGGTGACCA	701
Db	2593	CAGAGTGGTCTCAGAAAGGACCTGCGAGGCGCCACATGAGTTGCTGAAGACCCAGGTGACCA	2652
QY	702	AGAACAAAGCTGGGTGTCTGGCCCCCAGCGAGCTGACGGGTACCGGCGAGAGCTGGCCG	761
Db	2653	AGAACAAAGCTGGGTGTCTGGCCCCCAGCGAGCTGACGGGTACCGGCGAGAGCTGGCCG	2712
QY	762	AGCGTGCCGCTTGGGCTACCGAAGCTGCTTACCAACCTGTGGGCCCTCATCAACGAGG	821
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Db	2773	CGCTGCTGCATGATGAGCCCCCATGATCAAAAGCTCTCAGATCAACGGGAGGCCCTGAGTC	2832
QY	882	ATGGCCAGAACCCCTCTGCCCATCTA CTGTGCCCTCAACACCAAGCGGAGAGGCGCTGACCA	941
Db	2833	ATGGCCAGAACCCCTCTGCCCATCTA CTGTGCCCTCAACACCAAGCGGAGAGGCGCTGACCA	2892
QY	942	CTTTTGAATTTGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTGGCTTCCCCAAGTAGC	1001
Db	2893	CTTTTGAATTTGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTGGCTTCCCCAAGTAGC	2952
QY	1002	GGGCTTTCATCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATFGGGGCGAGCTGATGAAGA	1061
Db	2953	GGGCTTTCATCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATFGGGGCGAGCTGATGAAGA	3012
QY	1062	GGCTTCTGAGTCCGGCATCTGCTTCTTAGAAGTATCTGAGGCAACCTGTATGACAGCA	1121
Db	3013	GGCTTCTGAGTCCGGCATCTGCTTCTTAGAAGTATCTGAGGCAACCTGTATGACAGCA	3072
QY	1122	ACCTCCAGGACAGCTTTACTTGGGCGCTCAGAGCCCGACGAGTTCTGSGAACCGCTGGGTCA	1181
Db	3073	ACCTCCAGGACAGCTTTACTTGGGCGCTCAGAGCCCGACGAGTTCTGSGAACCGCTGGGTCA	3132
QY	1182	GGAAACAGGCCAACCTGAGCAAGGAGCAGGTCCCTCTTGAGATGAGAGAACCAACCT	1241
Db	3133	GGAAACAGGCCAACCTGAGCAAGGAGCAGGTCCCTCTTGAGATGAGAGAACCAACCT	3192
QY	1242	GAAACAGCGCGCAGATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCAATGGCCC	1301
Db	3193	GAAACAGCGCGCAGATAGCTGAGTTTTCACCGATCTTCTGACGTGGCGTCCAATGGCCC	3252
QY	1302	AGGCCACACATAATTTCTGGTGGCCCTCCATTTCCAAAGACTATCTTTCAGGATCTCTC	1361
Db	3253	AGGCCACACATAATTTCTGGTGGCCCTCCATTTCCAAAGACTATCTTTCAGGATCTCTC	3312
QY	1362	ACTTCTCCATAGGAAGCTACACTCTGGATGGGCTCCCCAAACAGCTGACACCTTCGG	1421
Db	3313	ACTTCTCCATAGGAAGCTACACTCTGGATGGGCTCCCCAAACAGCTGACACCTTCGG	3372
QY	1422	AGCCCCACCTGTGCTGCTGGATGTTGGCTCACTCATCAATACAGCTGCTGCCCTCC	1481
Db	3373	AGCCCCACCTGTGCTGCTGGATGTTGGCTCACTCATCAATACAGCTGCTGCCCTCC	3432
QY	1482	TGCAGGCCCATCGGGACGTGGACCTCATCTCTGCTATTGGACTACAACTCCACCGAGCCT	1541

[illegible]

/note= "No start codon shown"

FT US6482625-B1.
 XX 19-NOV-2002.
 XX 29-JUN-2001; 2001US-00895547.
 XX 24-JAN-1997; 97US-00788975.
 XX 13-DEC-1999; 99US-00460145.
 XX (GEM) GENETICS INST LLC.
 XX Kriz R, Song C;
 XX WPI; 2003-287361/28.
 XX DR P-PSDB; ABG76482.
 XX Novel purified calcium-independent cytosolic phospholipase A2-beta
 XX enzyme, useful for screening compounds having antiinflammatory activity
 XX mediated by the arachidonic acid cascade.
 XX Claim 1; Col 11-14; 19pp; English.
 XX The invention relates to a purified phospholipase enzyme (calcium-
 XX independent cytosolic phospholipase A 2-beta enzyme) peptide appearing as
 XX ABG76482 encoded by a polynucleotide appearing as ABX118883. The protein
 XX has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoyl
 XX -2-(1'-4C)-arachidonyl- phosphatidylcholine. cPLA2-beta is useful for
 XX assaying chemical agents for antiinflammatory activity mediated by the
 XX various components of the arachidonic acid cascade. cPLA2-beta is also
 XX useful in the development of polyclonal and monoclonal antibodies which
 XX are useful as research or diagnostic tools, and to study phospholipase
 XX A 2 activity and inflammatory conditions. The present sequence encodes a
 XX partial cPLA2-beta protein
 XX
 XX SQ Sequence 4183 BP; 983 A; 1177 C; 1168 G; 850 T; 0 U; 5 Other;
 Query Match 82.0%; Score 1806.2; DB 7; Length 4183;
 Best Local Similarity 98.1%; Pred. No. 0;
 Matches 1851; Conservative 0; Mismatches 3; Indels 33; Gaps 1;
 342 GACTGAGGAGCTGGCCCTGGCACTGGGCTTCGGGCTTCGAGGAGGAGGCTTCC 401
 2293 GACTGAGGAGCTGGCCCTGGCACTGGGCTTCGGGCTTCGAGGAGGAGGCTTCC 2352
 402 TGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 461
 2353 TGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2412
 462 ACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 521
 2413 ACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2472
 522 CAATGAGCTCCCTGTATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 581
 2473 CAATGAGCTCCCTGTATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2532
 582 TCTCCTACATCACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 641
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 642 CAGAGTGGTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 701
 2593 CAGAGTGGTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2652
 702 AGACAGAGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 761
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 762 AGCGTGGCCGCTTGGGCTACCCAGAGCTGCTTACCAACCAACCAACCAACCAAC 821
 2713 AGCGTGGCCGCTTGGGCTACCCAGAGCTGCTTACCAACCAACCAACCAACCAAC 2772

QY 822 CGCTGCTGATGATGAGCCCATGATCACAAGCTCTCAGATCAACCGGAGGAGGCTGAGTC 881
 DB 2773 CGCTGCTGATGATGAGCCCATGATCACAAGCTCTCAGATCAACCGGAGGAGGCTGAGTC 2832
 QY 882 ATGGCCAGAAACCTCTGCGCATCTACTGTGCCCTCAACACCAAAAGGAGGAGGCTGACCA 941
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 QY 942 CTTTGAATTTGGGAGTGGTGCAGTTCTCTCCCTACGAGTTCGGCTTCCCAAGTACG 1001
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 DB 3373 AGCCGCCACTGTGCTGTGATGTTGGTACTATCAATACAGGAGGAGGAGGAGGAGGAGGAG 3432
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 DB 3793 AGCTGTGACCTGACACATTAATGTTCTGCAACCAACCAACCAACCAACCAACCAACCAAC 3852

28

Fri Oct 8 10:22:36 2004

us-09-830-321a-5.rng

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QY 1933 CCTAATCTCATTCATTCCTCGCTGCTGAGTTGAGGTGGGAACGTGTCATCACGCAGTG 1992
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QY 1993 CTTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCAGGCTCCAGGCTGAGGGCTGGGAGCTC 2052
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QY 2053 CTTTGGCGCTCAGCAGTTTCAGTGGGTTAAGAGGCCAAGCCATTGTGTATATCACCC 2112
Db 1746 CTTTGGCGCTCAGCAGTTTCAGTGGGTTAAGAGGCCAAGCCATTGTGTATATCACCC 1805
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QY 2173 GATACATCACAGACTCATACAA 2195
Db 1866 GATACATCACAGACTCATACAA 1888

RESULT 13
ACD08100
ID ACD08100 standard; cdna; 1925 BP.
XX AC ACD08100;
XX XX
XX DT 12-AUG-2003 (first entry)
XX XX
XX DE cdna encoding novel human secreted protein #76.
XX KW Human; immunoglobulin G; IgG; fragment of crystallisation; FC;
XX KW immune system disorder; haematopoietic cell disorder;
XX KW immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
XX KW Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
XX KW blood coagulation disorder; blood platelet disorder; autoimmune disorder;
XX KW Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
XX KW glomerulonephritis; Grave's disease; allergic reaction; neoplasm;
XX KW graft-versus-host disease; hyperproliferative disorder;
XX KW infectious disease; nervous system disease; spinal cord disorder;
XX KW head trauma; stroke; tissue regeneration; congenital defect; trauma;
XX KW wound; burn; incision; ulcer; age disease; osteoporosis;
XX KW periodontal disease; liver failure; catabolism; anabolism; metabolism;
XX KW food additive; preservative; secreted protein; gene; ss.
XX OS Homo sapiens.
XX XX
XX PN US2003027132-A1.
XX XX
XX PD 06-FEB-2003.
XX XX
XX PF 04-SEP-1998; 98US-00148545.
XX XX
XX PR 07-MAR-1997; 97US-0038621P.
XX PR 07-MAR-1997; 97US-0040161P.
XX PR 07-MAR-1997; 97US-0040162P.
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XX PR 07-MAR-1997; 97US-0040626P.
XX PR 11-APR-1997; 97US-0043311P.
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PR 23-MAY-1997; 97US-0047492P.
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PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
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PR 23-MAY-1997; 97US-0047601P.
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PR 23-MAY-1997; 97US-0047613P.
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PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
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PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
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PR 05-SEP-1997; 97US-0057761P.
PR 06-MAR-1998; 98WO-US004482.

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PA	(ROSE//)	ROSEN C A.
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PA	(SOPF//)	SOPPET D R.
PA	(CART//)	CARTER K C.
PA	(BEDN//)	BEDNARIK D R.
PA	(ENDR//)	ENDRESS G A.
PA	(YUGG//)	YU G.
PA	(NIJJ//)	NI J.
PA	(FENG//)	FENG P.
PA	(YOUN//)	YOUNG P E.
PA	(GREE//)	GREENE J M.
PA	(FERR//)	FERRIE A M.
PA	(DUAN//)	DUAN R.
PA	(HUJU//)	HU J.
PA	(FLOR//)	FLORENCE K A.
PA	(OLSE//)	OLSEN H S.
PA	(EBNER//)	EBNER R.
PA	(BREW//)	BREWER L A.
PA	(SHIY//)	SHI Y.

PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Shi Y;

DR WPI; 2003-466138/44.
DR P-PSDB; ABO02008.

PPT Novel isolated human secreted HODA250 polypeptide useful for diagnosing or treating deficiencies or disorders of the immune system, autoimmune disorders, hyperproliferative disorders, and infectious diseases.

Claim 4; Page 130-131; 243pp; English.

The invention describes an isolated human secreted HODAZ50 polypeptide (I) comprising a sequence at least 95% identical to a sequence selected from polypeptide fragment of any one of the 123 polypeptide sequences (PS) fully defined in the specification and having biological activity, polypeptide domain or epitope of PS, secreted form of PS, full-length protein of PS, or variant, allelic variant or species homologue of PS. (I) or a polynucleotide (II) encoding (I) is useful for preventing, treating, or ameliorating a medical condition in a mammalian subject, (II) is also useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject. (I) is useful for identifying a binding partner which involves contacting the polypeptide with the binding partner and determining whether the binding partner affects the activity of the polypeptide. (I) or (II) is useful for diagnosing or treating deficiencies or disorders of the immune system, deficiencies or disorders of haematopoietic cells, to treat immunologic deficiency disorders, ataxia telangiectasia, HIV infection, Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood coagulation disorders, blood platelet disorders, autoimmune disorders (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis, dermatitis, glomerulonephritis, Grave's disease), allergic reactions, graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms located in the abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands), infectious diseases (e.g., viral, bacterial, fungal or parasitic infection), central and peripheral nervous system diseases (e.g., spinal cord disorders, head trauma or stroke), to differentiate, proliferate and attract cells leading to the regeneration of tissues to repair, replace or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g., osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV) is useful to modulate mammalian characteristics, to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilisation, and storage of energy, to change a mammal's mental state or physical state, or as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. This

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us-09-830-321a-5.rng

1366 CTCACATGGAAGCTACCACTCTGATGGCTCCCAACCAAGCTGACACCCCTCGAGCC 1425
1026 CTCACATGGAAGCTACCACTCTGATGGCTCCCAACCAAGCTGACACCCCTCGAGCC 1085
1426 CCACTGTGCTCTGATGATGTTGGCTACCTCATCAATACAGCTGCTGCCCTCTCTGCA 1485
1086 CCACTGTGCTCTGATGATGTTGGCTACCTCATCAATACAGCTGCTGCCCTCTCTGCA 1145
1486 GCCACTTCGGGACGCTGAGACCTCATCTCTGATGATGTTGGCTACCTCATCAATACAGCTGCTGCCCTCTCTGCA 1545
1146 GCCACTTCGGGACGCTGAGACCTCATCTCTGATGATGTTGGCTACCTCATCAATACAGCTGCTGCCCTCTCTGCA 1205
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1206 GCAGTTGCACTCTGCGGCGGCTTCTGCCAGGAGCAGGGATCCCGTTCCACCCATCTC 1265
1606 GCCAGCCCGGAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCAGCCCACTG 1665
1266 GCCAGCCCGGAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCAGCCCACTG 1325
1666 CCGCGAGCCCTGCGGTGCTGCACTTT----- 1693
1326 CCGCGAGCCCTGCGGTGCTGCACTTTCTCTGCTCAGCGACTCTTCCGGGAGTACTC 1385
1694 -TCTCTGGGTCGCGGGACACCCGAGGAGCGGAGCTGGGAGGTGAACCTGTCTTC 1752
1386 GGGCCCTTGGGTTCGGCGGACACCCGAGGAGCGGAGCTGGGAGGTGAACCTGTCTTC 1445
1753 ATCGGACTCTCCCTACCACTACAGAAAGGTGACCTACAGCCAGGAGCAGTGGGACAGCT 1812
1446 ATCGGACTCTCCCTACCACTACAGAAAGGTGACCTACAGCCAGGAGCAGTGGGACAGCT 1505
1813 GCTGCACCTGACATTTACATGCTGCAACACGAGGAGCAGCTGCTGGAGGCTCTGCG 1872
1506 GCTGCACCTGACATTTACATGCTGCAACACGAGGAGCAGCTGCTGGAGGCTCTGCG 1565
1873 CCAGGAGTGCAGCGGAGCGGAGCGAGCGAGCCCGGAGCTGATGGCGGGGCGGCTGCCACC 1932
1566 CCAGGAGTGCAGCGGAGCGGAGCGAGCGAGCGGAGCTGATGGCGGGGCGGCTGCCACC 1625
1933 CCTAACTCTCATTTCCCTGGCTGCTGAGTGCAGTGGGAACTGTCATCAGCAGTG 1992
1626 CCTAACTCTCATTTCCCTGGCTGCTGAGTGCAGTGGGAACTGTCATCAGCAGTG 1685
1993 CTT-CAGAGCTCGGCTCAGTGGCACTTCCAGGCTCCAGGCTGAGGCTGGAGCT 2051
1686 CTTNAGAGCTCGGCTCAGTGGCACTTCCAGGCTCCAGGCTGAGGCTGGAGCT 1745
2052 CCCTTGGCCTCAGCAGTTTGCAGTGGGTAAAGGAGGCGCAAGCCCATTTGTGTAATCACC 2111
1746 CCCTTGGCCTCAGCAGTTTGCAGTGGGTAAAGGAGGCGCAAGCCCATTTGTGTAATCACC 1805
2112 CAAACCCCGGCTGCTGCTGTTTCCCTTCTGGCTACCTCAGTAGTTGGAGCACT 2171
1806 CAAACCCCGGCTGCTGCTGTTTCCCTTCTGGCTACCTCAGTAGTTGGAGCACT 1865
2172 TGATACATCAGACTCATACAA 2195
1866 TGATACATCAGACTCATACAA 1889

RESULT 15

ACD08035 standard; cDNA; 1926 BP.

XX ACD08035;

XX 12-AUG-2003 (first entry)

XX cDNA encoding novel human secreted protein #11.

XX Human; immunoglobulin G; IgG; fragment of crystallisation; Fc;
XX immune system disorder; haematopoietic cell disorder;

immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
blood coagulation disorder; blood platelet disorder; autoimmune disorder;
Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
glomerulonephritis; Grave's disease; allergic reaction;
graft-versus-host disease; hyperproliferative disorder; neoplasm;
infectious disease; nervous system disease; spinal cord disorder;
head trauma; stroke; tissue regeneration; congenital defect; trauma;
wound; burn; incision; ulcer; age disease; osteoporosis;
periodontal disease; liver failure; catabolism; anabolism; metabolism;
food additive; preservative; secreted protein; gene; ss.

Homo sapiens.

US2003027132-A1.

06-FEB-2003.

04-SEP-1998; 98US-00148545.

07-MAR-1997; 97US-0038621P.

07-MAR-1997; 97US-0040161P.

07-MAR-1997; 97US-0040162P.

07-MAR-1997; 97US-0040163P.

07-MAR-1997; 97US-0040333P.

07-MAR-1997; 97US-0040334P.

07-MAR-1997; 97US-0040336P.

07-MAR-1997; 97US-0040626P.

11-APR-1997; 97US-0043311P.

11-APR-1997; 97US-0043312P.

11-APR-1997; 97US-0043313P.

11-APR-1997; 97US-0043314P.

11-APR-1997; 97US-0043315P.

11-APR-1997; 97US-0043568P.

11-APR-1997; 97US-0043569P.

11-APR-1997; 97US-0043576P.

11-APR-1997; 97US-0043578P.

11-APR-1997; 97US-0043580P.

11-APR-1997; 97US-0043669P.

11-APR-1997; 97US-0043670P.

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11-APR-1997; 97US-0043672P.

11-APR-1997; 97US-0043674P.

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23-MAY-1997; 97US-0047500P.

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23-MAY-1997; 97US-0047600P.

23-MAY-1997; 97US-0047601P.

23-MAY-1997; 97US-0047612P.

23-MAY-1997; 97US-0047613P.

23-MAY-1997; 97US-0047614P.

23-MAY-1997; 97US-0047615P.

23-MAY-1997; 97US-0047617P.

Fri Oct 8 10:22:36 2004

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Qy 766 TGCCCGCTTGGGCTACCAAGCTGTCTTACCAACCTGTGGGCCCTTATCAACAGGAGCGCT 825
Db 426 TGCCCGCTTGGGCTACCAAGCTGTCTTACCAACCTGTGGGCCCTTATCAACAGGAGCGCT 485
Qy 826 GGTGATGATGAGCCCCATGATCAAGAGCTGTCAATCAACGGGAGGCGCTGAGTCATGG 885
Db 486 GGTGATGATGAGCCCCATGATCAAGAGCTGTCAATCAACGGGAGGCGCTGAGTCATGG 545
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Db 546 CCAGAACCTCTGCCATCTACTGTGCTCCCTCAACACCAAGGCGAGAGCTGACCACTTT 605
Qy 946 TGAATTTGGGAGTGTGGAGTTCTCTCCCTACGAGGTGGCTTCCCAAGTACGGGCG 1005
Db 606 TGAATTTGGGAGTGTGGAGTTCTCTCCCTACGAGGTGGCTTCCCAAGTACGGGCG 665
Qy 1006 CTTTATCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGCGAGCTGATGAAGAGGCT 1065
Db 666 CTTTATCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGCGAGCTGATGAAGAGGCT 725
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Db 726 TCCGTGAGTCCCGCATCTGCTTCTTAGAAGTATCTGAGCAACCTGTATGAGAGGCT 785
Qy 1126 CCAGGACAGCTTATCTGAGGCTCTGAGGCCAGCCAGCTTCTGGGACCGCTGGGTGAGGAA 1185
Db 786 CCAGGACAGCTTATCTGAGGCTCTGAGGCCAGCCAGCTTCTGGGACCGCTGGGTGAGGAA 845
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Qy 1246 AGCCGCGAGATAGCTGAGTTTTCACCGATCTTCTGACGTGGGCTCCACTGGGCCAGGC 1305
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Db 1026 CTTACATGGAAGTACACTCTGAGTGGGCTCCCAACAGCTGACACCTCTGGAGCC 1085
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Db 1086 CCACCTGTGCTGAGTGTGGTACTCTCATCAATACAGCTGCCTGCCCTCTGCA 1145
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Db 1266 GCCCAGCCCCGAGAGAGCTCCAGCTCGGGAGTGCACACTTCTCGAACCCACCTG 1325
Qy 1666 CCCCGAGCCCCGCGGTGCTGACTTT----- 1693
Db 1326 CCCCGAGCCCCGCGGTGCTGACTTTCTCTGCTGAGGACTCTCTTCCGGAGTACTC 1385
Qy 1694 -TCTCTGGGTCGGGCGGACACCCGAGGAGCGGAGCTGGGGAGGTGAACCTGTCTC 1752
Db 1386 GGCCCTCTGGGGTCCGCGGACACCCGAGGAGGGGAGCTGGGGAGGTGAACCTGTCTC 1445
Qy 1753 ATCGGACTCTCCCTTACCACTACAGAGGTGAACCTACAGCAGGAGAGCTGACAGCT 1812
Db 1446 ATCGGACTCTCCCTTACCACTACAGAGGTGAACCTACAGCAGGAGAGCTGACAGCT 1505

Qy 1813 GCTGCACTGTACACATTAATGTCTGCAACAACAGGAGCAGCTGCTGGAGGCTCTGCG 1872
Db 1506 GCTGCACTGTACACATTAATGTCTGCAACAACAGGAGCAGCTGCTGGAGGCTCTGCG 1565
Qy 1873 CCAGGAGTGCAGCGGAGGCGGCGAGCGCAGGCGCCCACTGATGGCGGGGCCCTCTGCCACC 1932
Db 1566 CCAGGAGTGCAGCGGAGGCGGCGAGCGCAGGCGCCCACTGATGGCGGGGCCCTCTGCCACC 1625
Qy 1933 CCTAACTCTCATTTCTATTCCTTGGCTGCTGAGTTGAGGTGGGAACTGTCTATCAGCAGTG 1992
Db 1626 CTTAACTCTCATTTCTATTCCTTGGCTGCTGAGTTGAGGTGGGAACTGTCTATCAGCAGTG 1685
Qy 1993 CTTT-CAGAGCCTCGGCTCAGGTGGCACTGTCCAGGGTCCAGGCTGAGGCTGGGAGCT 2051
Db 1686 CTTTCAGAGCCTCGGCTCAGGTGGCACTGTCCAGGGTCCAGGCTGAGGCTGGGAGCT 1745
Qy 2052 CCGTTGGGCTCAGCAGTGTGGGTAAAGGAGGCCAAGCCCACTTTGTGTAATCAAC 2111
Db 1746 CCGTTGGGCTCAGCAGTGTGGGTAAAGGAGGCCAAGCCCACTTTGTGTAATCAAC 1805
Qy 2112 CAAAACCCCGGCTGTGCTGCTTTTCCCTTCTGCGTACCTTGAGTAGTTGGAGCACT 2171
Db 1806 CAAAACCCCGGCTGTGCTGCTTTTCCCTTCTGCGTACCTTGAGTAGTTGGAGCACT 1865
Qy 2172 TGATATATCACAGACTCATCAAAA 2195
Db 1866 TGATATATCACAGACTCATCAAAA 1889

Search completed: October 7, 2004, 13:34:49
Job time : 959.252 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2004, 11:15:59 ; Search time 8928.72 Seconds
(without alignments)
10698.960 Million cell updates/sec

Title: US-09-830-321A-5
Perfect score: 2204
Sequence: 1 catggtttggggcgagaga.....actcatcaaaaaaaaaa 2204

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
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- 21: em.or.*
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- 33: em.htg.mus.*
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- 35: em.htg.rtd.*
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- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2118.6	96.1	3038	9	AK124489	AK124489 Homo sapi
2	1816.8	82.4	3085	6	AR137923	AR137923 Sequence
3	1816.8	82.4	3085	6	AR137924	AR137924 Sequence
4	1816.8	82.4	3085	6	AR156370	AR156370 Sequence
5	1816.8	82.4	3085	6	AR156371	AR156371 Sequence
6	1816	82.4	3352	9	AF065215	AF065215 Homo sapi
7	1814	82.3	3193	9	BC013415	BC013415 Homo sapi
8	1806.2	82.0	2699	6	AR168355	AR168355 Sequence
9	1806.2	82.0	2699	6	AR255869	AR255869 Sequence
10	1806.2	82.0	3339	9	AF121908	AF121908 Homo sapi
11	1806.2	82.0	4183	6	AR168354	AR168354 Sequence
12	1806.2	82.0	4183	6	AR255868	AR255868 Sequence
13	1788.8	81.2	1925	6	AR352679	AR352679 Sequence
14	1788.8	81.2	1925	6	BD195624	BD195624 70 human
15	1777.8	80.7	1926	6	AR352614	AR352614 Sequence
16	1777.8	80.7	1926	6	BD195559	BD195559 70 human
17	1676.6	76.1	1818	6	AR352680	AR352680 Sequence
18	1676.6	76.1	1818	6	BD195625	BD195625 70 human
19	1422	64.5	7252	9	AF065216	AF065216 Homo sapi
20	1408.6	63.9	8517	6	AR137922	AR137922 Sequence
21	1408.6	63.9	8517	6	AR156369	AR156369 Sequence
22	1320.2	59.9	3775	9	HS080846	EX648318 Homo sapi
23	918.4	41.7	1712	10	BC042758	BC042758 Mus muscu
24	602	27.3	2409	6	AX417785	AX417785 Sequence
25	602	27.3	3197	6	AX402962	AX402962 Sequence
26	602	27.3	3587	9	AB090876	AB090876 Homo sapi
27	509.2	23.1	168413	2	AC009877	AC009877 Homo sapi
28	507.6	23.0	139376	9	AC020659	AC020659 Homo sapi
29	507.6	23.0	180304	2	AC012541	AC012541 Homo sapi
30	494.8	22.5	58152	2	AC087582	AC087582 Homo sapi
31	444.2	20.2	3998	9	HS080863	EX648482 Homo sapi
32	441	20.0	4066	9	AK127558	AK127558 Homo sapi
33	429.6	19.5	3879	6	AX512947	AX512947 Sequence
34	399.8	18.1	3370	9	BC035335	BC035335 Homo sapi
35	398.2	18.1	3460	6	BD141861	BD141861 Polypepti
36	393.2	17.8	3032	9	AK122623	AK122623 Homo sapi
37	385.8	17.5	2547	6	AX402959	AX402959 Sequence
38	380.2	17.3	4459	10	BC060600	BC060600 Mus muscu
39	365	16.6	2694	6	BD141893	BD141893 Polypepti
40	358.6	16.3	3006	10	BC039947	BC039947 Mus muscu
41	358.6	16.3	3112	6	BD141879	BD141879 Polypepti
42	336.2	15.3	2397	6	AX490840	AX490840 Sequence
43	261.6	11.9	1269	6	AX417778	AX417778 Sequence
44	217	9.8	421	11	G23044	G23044 human STS W
45	184.8	8.4	237806	2	AC097746	AC097746 Rattus no

ALIGNMENTS

RESULT 1
AK124489
LOCUS
DEFINITION
Homo sapiens cDNA FLJ42498 fis. clone BRACE203381, highly similar
to Homo sapiens phospholipase A2, group IVB (cytosolic) (FLA2G4B).
ACCESSION
AK124489.1 GI:34530282
VERSION
AK124489.1
KEYWORDS
oligo capping; fis (full insert sequence).
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M., Ozaki,K.,
Shimizu,F., Wakebe,H., Ono,T., Hishigaki,H., Watanabe,T.,

Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yanamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanenori,K.,
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahara,K., Masuho,Y., Nagai,K. and Isogai,T.
NEO human cDNA sequencing project

TITLE

JOURNAL

REFERENCE

AUTHORS

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QY 537 ATGGGAGCTGGCTGGCTGGCTGAAGAGCTGGGCTCTTGATTTGGCTTCCTACATCACG 596
DB 1350 ATGGGAGCTGGCTGGCTGGCTGAAGAGCTGGGCTCTTGATTTGGCTTCCTACATCACG 1409
QY 597 GGGGCTCGGGCTCACCTGGGCTTGGCCACCTTTATGAGGACCCAGAGTGGTCTCAGA 656
DB 1410 GGGGCTCGGGCTCACCTGGGCTTGGCCACCTTTATGAGGACCCAGAGTGGTCTCAGA 1469
QY 657 AGGACCTGGGAGGCGCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAACAGCTGGGTG 716
DB 1470 AGGACCTGGGAGGCGCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAACAGCTGGGTG 1529
QY 717 TGCTGGGCCCCAGCCAGCTGCAGCGGTACCCGAGAGCTGGCGAGCGTGGCCCTGG 776
DB 1530 TGCTGGGCCCCAGCCAGCTGCAGCGGTACCCGAGAGCTGGCGAGCGTGGCCCTGG 1589
QY 777 GCTACCCAGCTGCTTACCAACCTTGGGCTTATCAACGAGGCGCTGCTGCATGATG 836
DB 1590 GCTACCCAGCTGCTTACCAACCTTGGGCTTATCAACGAGGCGCTGCTGCATGATG 1649
QY 837 AGCCCATGATCAACAAGCTCTCAGATCAACGAGGCGCTGAGTCAATGCGCAGAACCTTC 896
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QY 837 TGCCCATCTAGTGGCTCCCTCAACCAAGGAGAGCTGACCACTTTTGAATTTGGG 956
DB 1710 TGCCCATCTAGTGGCTCCCTCAACCAAGGAGAGCTGACCACTTTTGAATTTGGG 1769
QY 957 AGTGTGGAGTCTCTCCCTACGAGTGGCTTCCCAAGTACGAGGCGCTTCATCCCT 1016
DB 1770 AGTGTGGAGTCTCTCCCTACGAGTGGCTTCCCAAGTACGAGGCGCTTCATCCCT 1829
QY 1017 CTGAGCTCTTTGGCTCCGAGTCTTTATGGGCGAGCTGATGAAGAGGCTTCCTGAGTCCC 1076
DB 1830 CTGAGCTCTTTGGCTCCGAGTCTTTATGGGCGAGCTGATGAAGAGGCTTCCTGAGTCCC 1889
QY 1077 GCATCTGCTTTAGAAAGTATCTGGAGCAACTGTATGAGCGCAACTCTCAGGACAGT 1136
DB 1890 GCATCTGCTTTAGAAAGTATCTGGAGCAACTGTATGAGCGCAACTCTCAGGACAGT 1949
QY 1137 TATCTGGGCTCAGAGCCAGCTTCTGGGCGCTGGGTTCAGGACAGGCGCAAC 1196
DB 1950 TATCTGGGCTCAGAGCCAGCTTCTGGGCGCTGGGTTCAGGACAGGCGCAAC 2009
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QY 1257 TAGCTGAGTTTTCACCGATCTTGAAGTGGCTTCACTGGGCGCTCCACTGGGCGGCAACATAAT 1316
DB 2070 TAGCTGAGTTTTCACCGATCTTGAAGTGGCTTCACTGGGCGCTCCACTGGGCGGCAACATAAT 2129
QY 1317 TCCTGGGCTGGCTCCATTTCCAAAGACTTCTTTCAGCATCTTCTCCATGGA 1376
DB 2130 TCCTGGGCTGGCTCCATTTCCAAAGACTTCTTTCAGCATCTTCTCCATGGA 2189
QY 1377 AAGCTACCACTCTGGATGGGCTTCCCAACAGCTGACCTCGGAGCGCCACTGTGCC 1436
DB 2190 AAGCTACCACTCTGGATGGGCTTCCCAACAGCTGACCTCGGAGCGCCACTGTGCC 2249
QY 1437 TGCTGAGTGGTGGCTTACCTCATATACAGTGGCTGGCTTCTGAGCGGCTTCGAG 1496
DB 2250 TGCTGAGTGGTGGCTTACCTCATATACAGTGGCTGGCTTCTGAGCGGCTTCGAG 2309
QY 1497 AGCTGAGCTCTCTGCTGCTTGGACTCAAACTCCAGGAGGCTTCCAGAGGCTTCGAG 1556
DB 2310 AGCTGAGCTCTCTGCTGCTTGGACTCAAACTCCAGGAGGCTTCCAGAGGCTTCGAG 2369
QY 1557 TCCTGGGCGGTTCTGCCAGGAGCGGAGTCCGTTCCCAAGCTTCGAGCGGCTTCGAG 1616
DB 2370 TCCTGGGCGGTTCTGCCAGGAGCGGAGTCCGTTCCCAAGCTTCGAGCGGCTTCGAG 2429
QY 1617 AAGAGCAGCTCCAGCTCGGAGTGCCACCTTCTCCAGAGGCTTCGAGCGGAGGCTTCGAG 1676

ORIGIN

Query Match

Best Local Similarity 96.1%; Score 2118.6; DB 9; Length 3038;

Matches 2181; Conservative 0; Mismatches 11; Indels 37; Gaps 2;

QY 1 CATGTTTGGGCGCAGAGGCGCAGGAGNACCAAGGAGAGAAAGGAGGAAATTCGCGC 60
DB 810 CATGTTTGGGCGCAGAGGCGCAGGAGNACCAAGGAGAGAAAGGAGGAGGAAATTCGCGC 869
QY 61 CTTTGGGTGGAAGCTGTATGGCTGGACCTTAAATGATCTTCGTAGAGTTCGCGCCAC 120
DB 870 CTTTGGGTGGAAGCTGTATGGCTGGACCTTAAATGATCTTCGTAGAGTTCGCGCCAC 929
QY 121 CCGTGGCTCTCTCTGAGAGAGTGGCTTCTACCTCAGACACAGAGGATTTGGTCT 180
DB 930 CCGTGGCTCTCTCTGAGAGAGTGGCTTCTACCTCAGACACAGAGGATTTGGTCT 989
QY 181 TTTCTGCCCGCCCTGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 236
DB 990 TTTCTGCCCGCCCTGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1049
QY 237 TCGCCAGAGCTGGAGTGAATGGGCTGATCTGGCTCACTGCAACCTCGGCTCTGGGT 296
DB 1050 TCGCCAGAGCTGGAGTGAATGGGCTGATCTGGCTCACTGCAACCTCGGCTCTGGGT 1109
QY 297 TCAAGCGATTCTCTGCTCAGCTCCGAGTAGCTGGGATACAGACTGAGGAGCTGG 356
DB 1110 TCAAGCGATTCTCTGCTCAGCTCCGAGTAGCTGGGATACAGACTGAGGAGCTGG 1169
QY 357 CCGTGGCATGGGCTTCGGGCTCTGTGCAGAGAGCAGGCGCTTCTTGGAGCAGGAGGAGC 416
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DEFINITION Sequence 4 from patent US 6242206.
ACCESSION AR156371

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REFERENCE 1 (bases 1 to 3085)
AUTHORS Chou,X.-C.C., Kramer,R.M., Pickard,R.T., Sharp,J.D. and Striffler,B.A.
TITLE Human phospholipase A2 and related nucleic acid compounds
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ACCESSION

BC013415

VERSION

BC013415.2 GI:33604011

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 3193)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,

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 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
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 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22386257
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 Strausberg, R.
 Direct Submission
 Submitted (31-AUG-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 On Aug 12, 2003 this sequence version replaced gi:16807142.
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 cDNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadnan@systemsbio.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
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 Db 1410 AGACTGAGGAGGAGGAGCAGGCTGGCGCTTGGAGGAGGCGCTTGCAGCTGGATGG 1469
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 Oy 640 CCCAGAGTGGTCTCAGAAGGAGCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGAC 699
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 Db 1650 CAAAGAACAGCTGGGTGGTGGCGCCCGCCAGCAGCTGCAGCGGTACCCGCGAGAGCTGGC 1709
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 Oy 1180 CAGGAACAGGCGCAACCTGGACAGGAGCAGGTCCCGCTTCTGAAGATAGAGAACACC 1239
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Qy	1694	-----TCTCTGGGTTCGGCGGACACCCGAGGAGCGCGAGCTGGGAGGTGAACCT	1746		
Db	2670	GTAATCGGCCCTCGGGTTCGGCGGACACCCGAGGAGCGCGAGCTGGGAGGTGAACCT	2729		
Qy	1747	GTCTTCAATCGGACCTCTCCCTACCACTACGAAGGTGACCTACAGCCAGGAGACGTGGA	1806		
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Qy	1807	CAAGCTGCTGCACCTGACACATTACAATGCTGCAACAAACAGGAGCAGCTGCTGGAGGC	1866		
Db	2790	CAAGCTGCTGCACCTGACACATTACAATGCTGCAACAAACAGGAGCAGCTGCTGGAGGC	2849		
Qy	1867	TCTGCGCCAGGCACTGCAGCGGAGCGGACGACGAGCCCACTGATGCGCGGGGCCCT	1926		
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Qy	1927	GCCACCCCTAACTCTCAATTCATTCCTGGCTGCTGAGTTGCAAGTGGGAACTGTCAATCAC	1986		
Db	2910	GCCACCCCTAACTCTCAATTCATTCCTGGCTGCTGAGTTGCAAGTGGGAACTGTCAATCAC	2969		
Qy	1987	GCACTGCTTCAGAGCTCGGGCTCAGGTGGCACTGTCCAGGGTCCAGGCTGAGGGCTGG	2046		
Db	2970	GCACTGCTTCAGAGCTCGGGCTCAGGTGGCACTGTCCAGGGTCCAGGCTGAGGGCTGG	3029		
Qy	2047	GAGTCCCTTGGCTCAGCAGTTTCAGTGGGGTAAGAGGGCCAAAGCCCAATTTGTGTAA	2106		
Db	3030	GAGTCCCTTGGCTCAGCAGTTTCAGTGGGGTAAGAGGGCCAAAGCCCAATTTGTGTAA	3089		
Qy	2107	TCACCCAAAACCCCGGCTGTGCTGTTTTCCTTCTGGCTACCTTGTAGTAGTTGGA	2166		
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ACCESSION	AR168355.1	GI:17904228			
VERSION	Unknown.				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2699)				
AUTHORS	Kriz, R. and Song, C.				
TITLE	Cytosolic phospholipase A2-Beta enzymes				
JOURNAL	Patent: US 6287838-A 3 11-SEP-2001;				
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Best Local Similarity	98.1%;	Pred. No. 0;			
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Qy	342	GACTGAGGAGCTGGCCGTGCGACTGCGCTTGGGCTTGGGCTGTCAGAGGAGCAGGCTTCC	401		
Db	809	GACTGAGGAGCTGGCCGTGCGACTGCGCTTGGGCTTGGGCTGTCAGAGGAGCAGGCTTCC	868		
Qy	402	TGAGCAGGAGGAAGCAGGTGTTGGCCGCGCTTGAAGCAGGCCCTTCAGCTGGATGGAG	461		
Db	869	TGAGCAGGAGGAAGCAGGTGTTGGCCGCGCTTGAAGCAGGCCCTTCAGCTGGATGGAG	928		
Qy	462	ACCTGAGCAGGAGATGAGATCCCAAGTGGTAGCTATTATGGCCACTGGTGGATCCCGG	521		

Db	929	ACCTGAGGAGGAGTGGATCCCACTGAGTGTAGTATATATGCGCACTGTGGTGGGATCCGGG	988
Qy	522	CAATGACTTCCTCTATGCGCAGCTGCTGGCTGAAAGAGCTGGGCTCTTTGATTGCG	581
Db	989	CAATGACTTCCTCTATGCGCAGCTGCTGGCTGAAAGAGCTGGGCTCTTTGATTGCG	1048
Qy	582	TCTCCTCATCATCACCGGGCTTCGGGCTTCCAGCTGGGCTTGGGCCAACTTTATGAGGACC	641
Db	1049	TCTCCTCATCATCACCGGGCTTCGGGCTTCCAGCTGGGCTTGGGCCAACTTTATGAGGACC	1108
Qy	642	CAGAGTGGTCTCAGAAAGACCTGGCAGGCGCCCACTGAGTTGCTGAAGACCCAGGTGACCA	701
Db	1109	CAGAGTGGTCTCAGAAAGACCTGGCAGGCGCCCACTGAGTTGCTGAAGACCCAGGTGACCA	1168
Qy	702	AGAAACAGCTGGGTGTCTGGCCCCCAGCCAGCTGCGAGCGGTACCGGAGGAGCTGGCGG	761
Db	1169	AGAAACAGCTGGGTGTCTGGCCCCCAGCCAGCTGCGAGCGGTACCGGAGGAGCTGGCGG	1228
Qy	762	AGCGTGGCCGCTTGGGCTACCAAGCTGCTTCAACAACTTGGGCCCTCATCAACGAGG	821
Db	1229	AGCGTGGCCGCTTGGGCTACCAAGCTGCTTCAACAACTTGGGCCCTCATCAACGAGG	1288
Qy	822	CGCTGCTGCATGATGAGCCCATGATCACAACTCTCAGATCAACGCGAGGCCCTGAGTGC	881
Db	1289	CGCTGCTGCATGATGAGCCCATGATCACAACTCTCAGATCAACGCGAGGCCCTGAGTGC	1348
Qy	882	ATGCGCAAAACCTCTGCCCCATCTACTGTGCCCCCTCAACACCAAGGGGAGGAGCTGACCA	941
Db	1349	ATGCGCAAAACCTCTGCCCCATCTACTGTGCCCCCTCAACACCAAGGGGAGGAGCTGACCA	1408
Qy	942	CTTTTGAATTTGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTGGGCTTCCCAAGTAGG	1001
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Qy	1002	GGGCTTTCATCCCTCTGAGCTCTTTGGCTCGAGTCTTTTATGGGCGAGCTGTGAAGA	1061
Db	1469	GGGCTTTCATCCCTCTGAGCTCTTTGGCTCGAGTCTTTTATGGGCGAGCTGTGAAGA	1528
Qy	1062	GGCTTCCTGAGTCCCGCATCTGCTTTTAGAGGTATCTGGAGCAACCTGTATGAGGCA	1121
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Qy	1122	ACCTCCAGGAGAGCTTATCTGGGCTCAGAGCCAGGCTTCTGGGACCGCTGGGTCA	1181
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Qy	1182	GGAAACAGGCAACCTGGAGAGGAGCTCCCTCTTGAAGATAGAAGAACCAACCTC	1241
Db	1649	GGAAACAGGCAACCTGGAGAGGAGCTCCCTCTTGAAGATAGAAGAACCAACCTC	1708
Qy	1242	CAACAGCGGAGAGTGTAGTGTGATTTTTCACCGATCTTCTGACGTGGGCTTCCAGTGGCC	1301
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Qy	1302	AGGCCACACATTAATTTCTGGTGGCTCCATTTTCCAAAGACTACTTTTACAGATCCCTC	1361
Db	1769	AGGCCACACATTAATTTCTGGTGGCTCCATTTTCCAAAGACTACTTTTACAGATCCCTC	1828
Qy	1362	ACTTCTCCACATGGAAAGCTACCTCTGGATGGGCTCCCAACCAAGCTGACACCTCCG	1421
Db	1829	ACTTCTCCACATGGAAAGCTACCTCTGGATGGGCTCCCAACCAAGCTGACACCTCCG	1888
Qy	1422	AGCCCCACCTGTGCTGCTGATGTTGGCTACCTCATCAATACAGCTGCTGCTGCTCCCTCC	1481
Db	1889	AGCCCCACCTGTGCTGCTGATGTTGGCTACCTCATCAATACAGCTGCTGCTGCTCCCTCC	1948
Qy	1482	TGAGGCCACTCGGAGCTGGACCTCATCTGCTGATTTGAGCTACACCTTCCACGAGGCT	1541
Db	1949	TGAGGCCACTCGGAGCTGGACCTCATCTGCTGATTTGAGCTACACCTTCCACGAGGCT	2008
Qy	1542	TCCAGCAGTTGAGCTTCCCTGGGCGGCTTCTGCGAGGAGGAGGAGTCCCTGCTTCCACCCA	1601
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 DEFINITION Sequence 3 from patent US 6482625.
 ACCESSION AR255869
 VERSION AR255869.1 GI:27305099
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 2699)
 AUTHORS Kriz,R. and Song,C.
 TITLE Cytosolic phospholipase A2-beta enzymes
 JOURNAL Patent: US 6482625-A 3 19-NOV-2002;
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 Location/Qualifiers
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 Best Local Similarity 98.1%; Pred. No. 0;
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 342 GACTGAGGAGCTGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTTCC 401
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Db	2609	ACCCAAACCCCGGCTGCTGCTTTTCCCTTCGCTGCTACCTTGAGTAGTGGAGC	2668
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TITLE	JOURNAL	source
FEATURES		
CDS		
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Query Match	82.0%; Score 1806.2; DB 9; Length 3339;	
Best Local Similarity	98.1%; Pred. No. 0;	
Matches 1851; Conservative	0; Mismatches 3; Indels 33; Gaps 1;	
QY	342	GACTCAGGAGCTGGCCCTGCGACTTGGGCTTCGGGCTTGCAGGAGCAGGCGCTTCC
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QY	402	TGAGCAGGAGGAGCAGGTGGTGGCGCGCTTGCAGGAGCAGGCGCTTGCAGTGGAG
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Kriz, R.W.		Direct Submission
Submitted (21-JAN-1999)		Genetics Institute, 87 Cambridge Park Drive, Cambridge, MA 02140, USA
Location/Qualifiers		
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ACCESSION AR168354
VERSION AR168354.1 GI:17904226
KEYWORDS SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4183)
AUTHORS Kriz, R. and Song, C.
TITLE Cytosolic phospholipase A2-Beta enzymes
JOURNAL Patent: US 6287838-A 1 11-SEP-2001;
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DEFINITION Sequence 1 from patent US 6482625.
ACCESSION AR255868
VERSION AR255868.1 GI:27305098
KEYWORDS
SOURCE Unknown.
ORGANISM Unkown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 4183)
Krish, R. and Song, C.
TITLE Cytosolic phospholipase A2-beta enzymes
JOURNAL Patent: US 6482625-A 1 19-NOV-2002;
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ACCESSION AR352679
VERSION AR352679.1 GI:33757937
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1925)
AUTHORS Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
Bednariak,D.P., Endress,G.A., Yu,G.-L., Ni,J., Peng,P., Young,P.E.,
Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.-S., Florence,K.A.,
Olsen,H.S., Ebner,K., Brewer,L.A. and Shi,Y.
TITLE Secreted protein H0DAZ50
JOURNAL Patent: US 6590075-A 86 08-JUL-2003;
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RESULT 14

BD195624

LOCUS

DEFINITION

70 human secreted proteins.

ACCESSION

BD195624

VERSION

BD195624.1

KEYWORDS

JP 200251990-A/85.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 1925)

AUTHORS

Ruben, S.M., Rosen, C.A., Fischer, C.L., Soppet, D.R., Carter, K.C.,

Bednarek, D.P., Endress, G.A., Yu, G.L., N.J., Feng, P., Young, P.E.,

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Lafleur, D.W., Li, Y., Zeng, Z. and Kyaw, H.

70 human secreted proteins

Patent: JP 200251990-A 85 02-JUL-2002;

HUMAN GENOME SCIENCES INC

OS Unidentified

PN JP 200251990-A/85

PD 02-JUL-2002

PF 06-MAR-1998 JP 1998538875

PR 07-MAR-1997 US 60/040162, 07-MAR-1997 US 60/040333 PR

07-MAR-1997 US 60/038621, 07-MAR-1997 US 60/040161 PR

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A ENDRESS,GUO LIANG						
PI YU,JIAN NI,						
PI PING FENG,PAUL E YOUNG,JOHN M GREENE,ANN						
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ACCESSION AR352614
VERSION AR352614.1 GI:33757872
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1926)
AUTHORS Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
Bednarek,D.P., Endress,G.A., Yu,G.-L., Ni,J., Feng,P., Young,P.E.,
Greene,J.M., Ferrite,A.M., Duan,R., Hu,J.-S., Florence,K.A.,
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TITLE Secreted protein HODA250

JOURNAL
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Patent: US 6590075-A 21 08-JUL-2003;

Location/Qualifiers

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source

ORIGIN

Query Match 80.7%; Score 1777.8; DB 6; Length 1926;

Best Local Similarity 97.9%; Pred. No. 0;

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;; FILING DATE: 19-MAR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gaylo, Paul J.
;; REGISTRATION NUMBER: 36,808
;; REFERENCE/DOCKET NUMBER: X-10610
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (317) 276-0756
;; TELEFAX: (317) 276-3861
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3085 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 48..2786
US-09-498-809-2

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; Sequence 1, Application US/09460145
; Patent No. 6287838
; GENERAL INFORMATION:
; APPLICANT: Kriz, Ron
; APPLICANT: Song, Chuansheng
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPID
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,145
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/788,975
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4183 base pairs

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73	EARLIER FILING DATE: 1997-06-06

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; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
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; SEQ ID NO 86
; LENGTH: 1925
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Fri Oct 8 10:22:37 2004

us-09-830-321a-5.rni

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RESULT 12
US-09-148-545-21
; Sequence 21, Application US/09148545
; Patent No. 6590075

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1926

Query Match 80.7%; Score 1777.8; DB 4; Length 1926;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1844; Conservative 1; Mismatches 4; Indels 35; Gaps 3;

Qy	347	AGGAGCTGGCCGCTGGCGACTGGGCTTCGGGCCCTGTG-CAGAGGAGCAGGCTTCCTGAG	405
Db	6	AGGAGCTGGCCGCTGGCGACTGGGCTTCGGGCCCTGTGCGCAGAGGAGCAGCCTTCCTGAG	65
Qy	406	CAGAGGAGCAGGTGGTGGCCCGGCGCTTGGAGGAGGCGCCCTGCAGCTGGATGGAGACCT	465
Db	66	CAGAGGAGCAGGTGGTGGCCCGGCGCTTGGAGGAGGCGCCCTGCAGCTGGATGGAGACCT	125
Qy	466	GCAGGAGGATGAGATCCAGTGGTATTTATGGCCACTGGTGGTGGGATCCGGGCAAT	525
Db	126	GCAGGAGGATGAGATCCAGTGGTATTTATGGCCACTGGTGGTGGGATCCGGGCAAT	185
Qy	526	GACTTCCTGTATGGGAGCTGGCTGGCCCTGAAGGAGCTGGGCTCTTGGATTCGCTC	585
Db	186	GACTTCCTGTATGGGAGCTGGCTGGCCCTGAAGGAGCTGGGCTCTTGGATTCGCTC	245

586 CTACATACCGGGGCTCGGGCTCCACCTGGGGCTTGGCCAACTTTATGAGGACCCAGA 645
246 CTACATACCGGGGCTCGGGCTCCACCTGGGGCTTGGCCAACTTTATGAGGACCCAGA 305
646 GTGGTCTCAGAAAGACTGGCAGGGGCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAA 705
306 GTGGTCTCAGAAAGACTGGCAGGGGCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAA 365
706 CAAGCTGGGGTGTGTGGCCCCCAGCCAGCTGACGCGGTACCGGAGGAGCTGGCGGAGCG 765
366 CAAGCTGGGGTGTGTGGCCCCCAGCCAGCTGACGCGGTACCGGAGGAGCTGGCGGAGCG 425
766 TGCCCGCTTGGGTACCCAGCTGCTTACCAACCTGTGGCCCTCATCAACGAGGGGCT 825
426 TGCCCGCTTGGGTACCCAGCTGCTTACCAACCTGTGGCCCTCATCAACGAGGGGCT 485
826 GCTGCATGATGAGCCCAAGCTCTCAGATCAACGGGAGGCGCTTGATCATGG 545
486 GCTGCATGATGAGCCCAAGCTCTCAGATCAACGGGAGGCGCTTGATCATGG 545
886 CCAGAACCTCTGCCCCATCTAATGTGCGCTCAACACCAAGGGGAGAGCCCTGACCACTTT 945
546 CCAGAACCTCTGCCCCATCTAATGTGCGCTCAACACCAAGGGGAGAGCCCTGACCACTTT 605
946 TGAATTTGGGAGTGGTGGAGTTCTCTCCCTACGAGTCTGGCTTCCCAAGTACGGGGC 665
606 TGAATTTGGGAGTGGTGGAGTTCTCTCCCTACGAGTCTGGCTTCCCAAGTACGGGGC 665
1006 CTTTCATCCCTCTGAGCTCTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGCT 1065
666 CTTTCATCCCTCTGAGCTCTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGCT 725
1066 TCCTGAGTCCCGCATCTGCTTTCTTAGAAGGTATCTGGAGCAACCTGTATGAGCCAACT 1125
726 TCCTGAGTCCCGCATCTGCTTTCTTAGAAGGTATCTGGAGCAACCTGTATGAGCCAACT 785
1126 CCAGAGACTTATCTGGGCTCAGCCAGCCAGCTTCTGGGACCGCTGGGTGAGGAA 1185
786 CCAGAGACTTATCTGGGCTCAGCCAGCCAGCTTCTGGGACCGCTGGGTGAGGAA 845
1186 CCAGGCCAACTGGACAAGGAGCAGTCCCTCTCTGAAGATAGAGAACAACCCCTCAAC 1245
846 CCAGGCCAACTGGACAAGGAGCAGTCCCTCTCTGAAGATAGAGAACAACCCCTCAAC 905
1246 AGCCGCGAGAAATAGTGTGATTTTCCAGTCTTCTGAGTGGCTCCACTGGCCGAGGC 1305
906 AGCCGCGAGAAATAGTGTGATTTTCCAGTCTTCTGAGTGGCTCCACTGGCCGAGGC 965
1306 CACACATAATTTCTGGTGGGCTCCATTTCCAAAAGACTACTTTACGATCCTCACTT 1365
966 CACACATAATTTCTGGTGGGCTCCATTTCCAAAAGACTACTTTACGATCCTCACTT 1025
1366 CTTCCATGGAAGTACCACTCTGGATGGGCTCCCAACCAAGCTGACACCCCTGGAGCC 1425
1026 CTTCCATGGAAGTACCACTCTGGATGGGCTCCCAACCAAGCTGACACCCCTGGAGCC 1085
1426 CCACTGTGCTGCTGGATGTTGGCTACCTCATCAATACAGTGTGCTGCTGCTGCTGCA 1485
1086 CCACTGTGCTGCTGGATGTTGGCTACCTCATCAATACAGTGTGCTGCTGCTGCTGCA 1145
1486 GCCCATCTGGGAGCTGAGCTCATCTGTCATTTGGACTACAACTCCAGGAGCCCTTCCA 1545
1146 GCCCATCTGGGAGCTGAGCTCATCTGTCATTTGGACTACAACTCCAGGAGCCCTTCCA 1205
1546 GCAGTTGCACTCTCTGGGCGGGTCTTCCAGGAGCAGGGGATCCCGTTCACACCCATCTC 1605
1206 GCAGTTGCACTCTCTGGGCGGGTCTTCCAGGAGCAGGGGATCCCGTTCACACCCATCTC 1265
1606 GCCAGCCCGAAGAGAGCTCCAGCTCGGAGTGCACACCTTCTCCGAGCCCACTG 1665
1266 GCCAGCCCGAAGAGAGCTCCAGCTCGGAGTGCACACCTTCTCCGAGCCCACTG 1325
1666 CCCGGAGGCCCTGGTGTGCACTTT----- 1693

1326 CCCCAGAGCCCTGCGTCTGCACCTTTCTCTGGTCAGGACTCTCTTCGGGAGTACTC 1385
1694 -TCCTCTGGGTCCGGCGGACACCCGAGGAGGGCGAGCTGGGAGGTGAACCTGTCTTC 1752
1386 GGGCCCTGGGTCCGGCGGACACCCGAGGAGGGCGAGCTGGGAGGTGAACCTGTCTTC 1445
1753 ATCGGACTCTCCCTACCACTACACGAAAGTGAACCTACGACGAGGAGGACCTGACAGCT 1812
1446 ATCGGACTCTCCCTACCACTACACGAAAGTGAACCTACGACGAGGAGGACCTGACAGCT 1505
1813 GCTGCACCTGACACATTTACAACTGCTGCAACCAACGAGGAGGAGCTGCTGAGGCTCTGCG 1872
1506 GCTGCACCTGACACATTTACAACTGCTGCAACCAACGAGGAGGAGCTGCTGAGGCTCTGCG 1565
1873 CCAGGAGTGCAGCGAGGGCGGAGCGAGCGGCCCACTGATGGCGGGGCCCTTGCACAC 1932
1566 CCAGGAGTGCAGCGAGGGCGGAGCGAGCGGCCCACTGATGGCGGGGCCCTTGCACAC 1625
1933 CCTAAGTCTCATTCATTCCTGCTGCTGAGTTGCTGAGTGGGAACTGTCTACGCGAGTG 1992
1626 CCTAAGTCTCATTCATTCCTGCTGCTGAGTTGCTGAGTGGGAACTGTCTACGCGAGTG 1685
1993 CTT-CAGAGCTCGGGCTCAGGTGGCACTGTCCAGGCTCCAGGCTCAGGCTCGGAGCT 2051
1686 CTTNCAGAGCTCGGGCTCAGGTGGCACTGTCCAGGCTCCAGGCTCAGGCTCGGAGCT 1745
2052 CCCTTGGCGCTCAGCAGTTTGCAGTGGGGTAAAGAGGCGCAAGCCCACTTGTGTAATCACC 2111
1746 CCCTTGGCGCTCAGCAGTTTGCAGTGGGGTAAAGAGGCGCAAGCCCACTTGTGTAATCACC 1805
2112 CAAAACCCCGGCTGTGCTGCTTCCCTTCTGCGTACCTTGGAGTGTGGAGCACT 2171
1806 CAAAACCCCGGCTGTGCTGCTTCCCTTCTGCGTACCTTGGAGTGTGGAGCACT 1865
2172 TGATACATCAGACTCATACAA 2195
1866 TGATACATCAGACTCATACAA 1889

RESULT 13
US-09-148-545-87/c
; Sequence 87, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001PI
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597

1	EARLIER APPLICATION NUMBER: 60/056,633
2	EARLIER FILING DATE: 1997-08-22
3	EARLIER APPLICATION NUMBER: 60/056,878
4	EARLIER FILING DATE: 1997-08-22
5	EARLIER APPLICATION NUMBER: 60/056,662
6	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,872
8	EARLIER FILING DATE: 1997-08-22
9	EARLIER APPLICATION NUMBER: 60/056,882
10	EARLIER FILING DATE: 1997-08-22
11	EARLIER APPLICATION NUMBER: 60/056,637
12	EARLIER FILING DATE: 1997-08-22
13	EARLIER APPLICATION NUMBER: 60/056,903
14	EARLIER FILING DATE: 1997-08-22
15	EARLIER APPLICATION NUMBER: 60/056,888
16	EARLIER FILING DATE: 1997-08-22
17	EARLIER APPLICATION NUMBER: 60/056,879
18	EARLIER FILING DATE: 1997-08-22
19	EARLIER APPLICATION NUMBER: 60/056,880
20	EARLIER FILING DATE: 1997-08-22
21	EARLIER APPLICATION NUMBER: 60/056,894
22	EARLIER FILING DATE: 1997-08-22
23	EARLIER APPLICATION NUMBER: 60/056,911
24	EARLIER FILING DATE: 1997-08-22
25	EARLIER APPLICATION NUMBER: 60/056,636
26	EARLIER FILING DATE: 1997-08-22
27	EARLIER APPLICATION NUMBER: 60/056,874
28	EARLIER FILING DATE: 1997-08-22
29	EARLIER APPLICATION NUMBER: 60/056,910
30	EARLIER FILING DATE: 1997-08-22
31	EARLIER APPLICATION NUMBER: 60/056,864
32	EARLIER FILING DATE: 1997-08-22
33	EARLIER APPLICATION NUMBER: 60/056,631
34	EARLIER FILING DATE: 1997-08-22
35	EARLIER APPLICATION NUMBER: 60/047,595
36	EARLIER FILING DATE: 1997-08-23
37	EARLIER APPLICATION NUMBER: 60/057,761
38	EARLIER FILING DATE: 05-Sep-1997
39	EARLIER APPLICATION NUMBER: 60/047,599
40	EARLIER FILING DATE: 1997-05-23
41	EARLIER APPLICATION NUMBER: 60/047,588
42	EARLIER FILING DATE: 1997-05-23
43	EARLIER APPLICATION NUMBER: 60/047,585
44	EARLIER FILING DATE: 1997-05-23
45	EARLIER APPLICATION NUMBER: 60/047,586
46	EARLIER FILING DATE: 1997-05-23
47	EARLIER APPLICATION NUMBER: 60/047,590
48	EARLIER FILING DATE: 1997-05-23
49	EARLIER APPLICATION NUMBER: 60/047,594
50	EARLIER FILING DATE: 1997-05-23
51	EARLIER APPLICATION NUMBER: 60/047,589
52	EARLIER FILING DATE: 1997-05-23
53	EARLIER APPLICATION NUMBER: 60/047,593
54	EARLIER FILING DATE: 1997-05-23
55	EARLIER APPLICATION NUMBER: 60/047,614
56	EARLIER FILING DATE: 1997-05-23
57	EARLIER APPLICATION NUMBER: 60/043,578
58	EARLIER FILING DATE: 1997-04-11
59	EARLIER APPLICATION NUMBER: 60/043,576
60	EARLIER FILING DATE: 1997-04-11
61	EARLIER APPLICATION NUMBER: 60/047,501
62	EARLIER FILING DATE: 1997-05-23
63	EARLIER APPLICATION NUMBER: 60/043,670
64	EARLIER FILING DATE: 1997-04-11
65	EARLIER APPLICATION NUMBER: 60/056,632
66	EARLIER FILING DATE: 1997-08-22
67	EARLIER APPLICATION NUMBER: 60/056,664
68	EARLIER FILING DATE: 1997-08-22
69	EARLIER APPLICATION NUMBER: 60/056,876

[illegible]

Db 78 TTGAGTAGTTGGAGCACTTGATACATYACAGACTCATAMAAAAA 28

RESULT 14

US-08-827-208-1
; Sequence 1, Application US/08827208
; Patent No. 6025178
; GENERAL INFORMATION:
; APPLICANT: Chiou, Xue-Chiou C.
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Striffler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,208
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/014,608
; FILING DATE: 29-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,264
; FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1611..2063
; FEATURE:
; NAME/KEY: exon
; LOCATION: 5315..6045
; FEATURE:
; NAME/KEY: exon
; LOCATION: 6143..6758
; FEATURE:
; NAME/KEY: exon
; LOCATION: 7075..7317
; FEATURE:
; NAME/KEY: exon
; LOCATION: 7473..8499
US-08-827-208-1

Query Match 63.9%; Score 1408.6; DB 3; Length 8517;
Best Local Similarity 79.3%; Pred. No. 0;
Matches 1957; Conservative 0; Mismatches 4; Indels 506; Gaps 4;

QY	Db	244	6045	304	6105	364	6165	424	6225	483	6285	543	6345	603	6405	663	6465	723	6525	783	6585	843	6645	903	6705	956	6765	956	6825	956	6885	956	6945	956	7005	956	7065	1006			
QY	Db	GGCTGGAGTGCANTGGCGTGATCTTGCTCAGTGCACCTCGCGCTCTGGGTTCAAGCG	GGCTGGAGTGCANTGGCGTGATCTTGCTCAGTGCACCTCGCGCTCTGGGTTCAAGCG	ATTCTCTCTGCTCAGCTCCCGAGTAGCTGGGATTACAGACTGAGGAGCTGGCGGTGCG	ATTCTCTCTGCTCAGCTCCCGAGTAGCTGGGATTACAGACTGAGGAGCTGGCGGTGCG	ACTGGGCTTCGGGCCCTGTGACAGGAGCAGGCTTCTGAGCAGGAGGAGGAGGAGT	ACTGGGCTTCGGGCCCTGTGACAGGAGCAGGCTTCTGAGCAGGAGGAGGAGGAGT	GCGCGGCGCTTGGAGCAGGCGCTTCTGAGATGAGACCTGTCAGGAGATGAGAT-CC	GCGCGGCGCTTGGAGCAGGCGCTTCTGAGATGAGACCTGTCAGGAGATGAGAT-CC	CAGTGTAGCTATTATGGCCACTGGTGGTGGGATCGGGCAATGACTTCCCTGTATGGGC	CAGTGTAGCTATTATGGCCACTGGTGGTGGGATCGGGCAATGACTTCCCTGTATGGGC	AGCTGGCTGGCCTGAAGGAGCTGGGCTTCTTGGATTGGCTCTCTACATCACCGGGCCT	AGCTGGCTGGCCTGAAGGAGCTGGGCTTCTTGGATTGGCTCTCTACATCACCGGGCCT	CGGGCTCCACCTGGGCTTGGCCAACTTTATGAGACCCAGAGTGGTCTCAGAAAGACC	CGGGCTCCACCTGGGCTTGGCCAACTTTATGAGACCCAGAGTGGTCTCAGAAAGACC	TGGCAGGGGCCCACTGAGTGTGTAAGACCCAGGTGACCAAGAACAGCTGGGTGCTGG	TGGCAGGGGCCCACTGAGTGTGTAAGACCCAGGTGACCAAGAACAGCTGGGTGCTGG	CCCCCAGCAGCTGCAGCGGTACCGGAGGAGCTGGCGGAGCTGCGGCTTGGGCTACC	CCCCCAGCAGCTGCAGCGGTACCGGAGGAGCTGGCGGAGCTGCGGCTTGGGCTACC	CAAGCTGCTTCCACCACTGTGGGCTTCAATCAAGAGCGGCTGCTGATGAGCCCC	CAAGCTGCTTCCACCACTGTGGGCTTCAATCAAGAGCGGCTGCTGATGAGCCCC	ATGATCAAGCTCTCAGATCAACCGGAGGCTTCAATGAGTGCATGATGAGCCCC	ATGATCAAGCTCTCAGATCAACCGGAGGCTTCAATGAGTGCATGATGAGCCCC	TCTACTGTGCGCTCAACCAAGGAGGAGCTGACCACTTTTGAATTTGGG	TCTACTGTGCGCTCAACCAAGGAGGAGCTGACCACTTTTGAATTTGGG	-----	GGCCCAAGAGCTGAGACCTGTGCGCTTGCAGTTGGTGAATAGGGGAGAACGAGACTG	-----	TGTGAGATTGAGATGTCACACCACTCTCTGAGCCAGGCTCCCGTGTCTTCTGAGA	-----	CCGCACTTACCAGGCTCCCTCAGCCCTTGGGAGGAGGAGGAGGAGGAGGAGTAT	-----	GCAGAAAGCCAGGCCACAGGCTTGGGCTCTGCTGCTCAGTGCCTTAAAGCAAAAC	-----	CTTGGCTGGGTTGGGTTGGTGGCTTAAAGGCTCTGACCATGAGGCTGAGGCTGG	-----	-----GAGTGTGCGAGTTCTCTCCCTACGAGGCTGGCTTCCCAAGTACGGGC	-----	ACTCTTCACAGAGTGTGCGAGTTCTCTCCCTACGAGGCTGGCTTCCCAAGTACGGGC	-----	CTTCATCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGAGCTGATGAGAGGCT

Db	7125	CTTATCCCTCTGAGCTCTTTGGCTCCGAGTCTTTATGGGCGAGCTGATGAGAGGCT	7184
QY	1066	TCTGAGTCCCGCATCTGCTCTTTAGAGGTATCTGAGCAACCTGTATGAGCGCAACCT	1125
Db	7185	TCTGAGTCCCGCATCTGCTCTTTAGAGGTATCTGAGCAACCTGTATGAGCGCAACCT	7244
QY	1126	CAAGGACAGTTTATCTGAGGCTCAGAGCCAGCGAGTTCTGGAGCCGCTGGGTGAGGAA	1185
Db	7245	CAAGGACAGTTTATCTGAGGCTCAGAGCCAGCGAGTTCTGGAGCCGCTGGGTGAGGAA	7304
QY	1186	CAAGGCAACCTG-----	1198
Db	7305	CCAGGCAACCTGGGTAAGTGTCTCCGGGCCCTTCATAAGGGTGCCAGGGGCGAGCCAGCT	7364
QY	1199	-----	1198
Db	7365	GGGCTGCACACAGGGGGGGGGTTCCACACCTCTTCCCTCCAGGGTCACCAACAGG	7424
QY	1199	-----GACAAGGAGCAG	1210
Db	7425	TGGGATAAAGGTGAGAGTCCCATTTTCCCCACCTTGCTGTAGACAGGAGCAG	7484
QY	1211	GTCCCTCTCTGAAGATAGAAAGAACCCCTCAACAGCGCGGAGAGTGTGAGTTTTC	1270
Db	7485	GTCCCTCTCTGAAGATAGAAAGAACCCCTCAACAGCGCGGAGAGTGTGAGTTTTC	7544
QY	1271	ACCGATCTTCTGAGTGGGCTCCAGTGGCCAGGCGCACATATTTCTCGTGGGCTC	1330
Db	7545	ACCGATCTTCTGAGTGGGCTCCAGTGGCCAGGCGCACATATTTCTCGTGGGCTC	7604
QY	1331	CATTTCACAAGACTATTTTACATCTCTCCATGCTTCCATGAGAAAGCTTACCACTCTG	1390
Db	7605	CATTTCACAAGACTATTTTACATCTCTCCATGAGAAAGCTTACCACTCTG	7664
QY	1391	GATGGCTCCCAACAGCTGACACCTCGGAGCCCACTGTGCTCTGCTGATGTTGGC	1450
Db	7665	GATGGCTCCCAACAGCTGACACCTCGGAGCCCACTGTGCTCTGCTGATGTTGGC	7724
QY	1451	TACCTCATCAATPACAGTGGCTGCTGCTCTGAGGCCATCTGCGGAGCTGAGACTATC	1510
Db	7725	TACCTCATCAATPACAGTGGCTGCTGCTCTGAGGCCATCTGCGGAGCTGAGACTATC	7784
QY	1511	CTGTCTTGGACTACAACCTCACAGGAGCTTCCAGAGCTTCCAGCTCTTGGGCGGTTTC	1570
Db	7785	CTGTCTTGGACTACAACCTCACAGGAGCTTCCAGAGCTTCCAGCTCTTGGGCGGTTTC	7844
QY	1571	TGCCAGGAGCAGGGATCCCGTTCCCAACCCATCTCGCCAGCCCGGAGAGAGCTCCAG	1630
Db	7845	TGCCAGGAGCAGGGATCCCGTTCCCAACCCATCTCGCCAGCCCGGAGAGAGCTCCAG	7904
QY	1631	CCTCGGAGTGCCACACCTTCTCGACCCCACTGCGCCGAGCCCTGCGGTGCTGCAC	1690
Db	7905	CCTCGGAGTGCCACACCTTCTCGACCCCACTGCGCCGAGCCCTGCGGTGCTGCAC	7964
QY	1691	TTTT-----CCTCGGGTCCGCGGACACCC	1717
Db	7965	TTTTCTCTGTCAGCAGCTCTTCCGGAGTACTCGGCCCTTGGGTCGCGGACACCC	8024
QY	1718	GAGGAGCGGAGCTGGGAGGTGAACCTGTCTTCTCATCGGACTCTCCCTACCACTACAG	1777
Db	8025	GAGGAGCGGAGCTGGGAGGTGAACCTGTCTTCTCATCGGACTCTCCCTACCACTACAG	8084
QY	1778	AGGTGACCTACAGCAGGAGCTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1837
Db	8085	AGGTGACCTACAGCAGGAGCTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	8144
QY	1838	TGCAACAAACAGGAGCAGCTGCTGGAGGCTCTGCGCAGGAGCTGAGCGGAGCGGAG	1897
Db	8145	TGCAACAAACAGGAGCAGCTGCTGGAGGCTCTGCGCAGGAGCTGAGCGGAGCGGAG	8204
QY	1898	CGCAGGCGGAGCTGATGGCGGGGCGGCTTCCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1957

RESULT 15

US-09-500-358-1
; Sequence 1, Application US/09500358
; Patent No. 6197569

GENERAL INFORMATION:

APPLICANT: Chiou, Xue-Chiou C.
APPLICANT: Kramer, Ruth M.
APPLICANT: Pickard, Richard T.
APPLICANT: Sharp, John D.
APPLICANT: Striffler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,358
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/827,208
FILING DATE: 28-MAR-1997
APPLICATION NUMBER: US 60/014,608
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:

NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

	; MOLECULE TYPE:	DNA (genomic)
	; FEATURE:	
	; NAME/KEY:	exon
	; LOCATION:	1611..2063
	; FEATURE:	
	; NAME/KEY:	exon
	; LOCATION:	5315..6045
	; FEATURE:	
	; NAME/KEY:	exon
	; LOCATION:	6143..6758
	; FEATURE:	
	; NAME/KEY:	exon
	; LOCATION:	7075..7317
	; FEATURE:	
	; NAME/KEY:	exon
	; LOCATION:	7473..8499
	US-09-500-358-1	
	Query Match	63.9%; Score 1408.6; DB 3; Length 8517;
	Best Local Similarity	79.3%; Pred. No. 0;
	Matches 1957; Conservative	0; Mismatches 4; Indels 506; Gaps 4;
QY	244	GGCTGGAGTGCATATGCGCNGATTGTGGCTCACTGCAACCTCGCCTCTGGGGTTCAAAGC 303
Db	6045	GGCTGGAGTGCATATGCGTGATCTTGGTCATCTGAACCTCCGCTCTGGGGTTCAAAGC 6104
QY	304	ATTCTCTGCCCTCAGCTCCCGAGTAGCTGGGATTACAGACTGAGGGAGCTGGCCCTGCG 363
Db	6105	ATTCTCTGCCCTCAGCTCCCGAGTAGCTGGGATTACAGACTGAGGGAGCTGGCCCTGCG 6164
QY	364	ACTGGGCTTCGGGCCCTGTGCAGAGGACAGGCCCTTCTGAGCAGGAGGAAGCAGGTGCT 423
Db	6165	ACTGGGCTTCGGGCCCTGTGCAGAGGACAGGCCCTTCTGAGCAGGAGGAAGCAGGTGCT 6224
QY	424	GCCC CGGCCCTT GAGCGAGGCCCT GCAGCTGGATGGAGCTGAGAGCTGCGAGGATGAGAT - CC 482
Db	6225	GCC CGCGCCCT TGAGCGAGGCCCT TCGAGCTGGATGGAGCTGCGAGGATGAGATACC 6284
QY	483	CAGTGTAGCTATTATGSCCACTCTGGTGGGATCCGGGCAATGACTTCCTCTATGGGC 542
Db	6285	CAGTGTAGCTATTATGSCCACTCTGGTGGGATCCGGGCAATGACTTCCTCTATGGGC 6344
QY	543	AGCTGGCTGGCCTGAAGSAGCTGGCCCTCTTGATTTGCGTCTCTACATCACCGGGCCCT 602
Db	6345	AGCTGGCTGGCCTGAAGSAGCTGGCCCTCTTGATTTGCGTCTCTACATCACCGGGCCCT 6404
QY	603	CGGSCTCCACTCGGCCCTTGSCCAACTTTATGAGNACCCAGAGTGGTCTCAAGAGACC 662
Db	6405	CGGSCTCCA CTGGGCCCTTGSCCAACTTTATGAGNACCCAGAGTGGTCTCAAGAGACC 6464
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GenCore version 5.1.6
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Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1777.8	80.7	1926	10	US-09-148-545-21
7	1676.6	76.1	1818	9	US-09-981-876-87
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16	358.6	16.3	3112	16	US-10-380-873B-23	Sequence 23, Appl
17	235.6	10.7	554	10	US-09-918-995-28234	Sequence 28234, A
18	172.4	7.8	174	9	US-09-880-107-3899	Sequence 3899, Ap
19	166.6	7.6	556	13	US-10-296-115-178	Sequence 178, App
20	150	6.8	1519	16	US-10-380-873B-4	Sequence 4, Appli
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22	136.8	6.2	323	16	US-10-027-632-13940	Sequence 13940, A
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24	131.8	6.0	31868	17	US-10-444-795B-808	Sequence 808, App
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26	131.8	6.0	300000	17	US-10-703-210-33	Sequence 33, Appl
27	130.8	5.9	11853	16	US-10-074-024-739	Sequence 739, App
28	130.6	5.9	9474	9	US-09-764-878-372	Sequence 372, App
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32	130.2	5.9	186391	13	US-10-087-192-136	Sequence 136, App
33	129.8	5.9	32433	12	US-10-052-482-136	Sequence 334, App
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36	129.8	5.9	201986	13	US-10-087-192-874	Sequence 12145, A
37	129.6	5.9	201	17	US-10-741-601-12145	Sequence 252450,
38	129.6	5.9	1245	13	US-10-027-632-252450	Sequence 3, Appli
39	129.6	5.9	1245	16	US-10-027-632-252450	Sequence 11, Appl
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41	129.6	5.9	77992	15	US-10-225-810-11	Sequence 26, Appl
42	129.6	5.9	86081	17	US-10-741-601-5640	Sequence 568, App
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ALIGNMENTS

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; Sequence 3, Application US/10266388
; Publication NO. US20030124702A1
; GENERAL INFORMATION:
; APPLICANT: Kriz, Ron
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/266,388
; FILING DATE: 07-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,547
; FILING DATE: 29-Jun-2001
; APPLICATION NUMBER: 09/460,145
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851

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us-09-830-321a-5.rnpb

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Sequence 86, Application US/09981876
Patent No. US20020164669A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
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CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/148,545
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
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;; PRIOR FILING DATE: 1997-08-22
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Db 1626 CTTACTCTCATTCATCTCCCTGGCTGCTGAGTGGAGTGGAACTGTATCAGCAGTG 1685
QY 1993 CTTTCAGAGCTCGGGCTCAGGTGGCACTGTCCAGGGTCCAGGCTGAGGGCTGGAGCTC 2052
Db 1686 CTTTCAGAGCTCGGGCTCAGGTGGCACTGTCCAGGGTCCAGGCTGAGGGCTGGAGCTC 1745
QY 2053 CTTTGGGCTCAGCAGTTTGCAGTGGGTAAAGAGGCGGAGCCCATTTGTGTAATCACCC 2112
Db 1746 CTTTGGGCTCAGCAGTTTGCAGTGGGTAAAGAGGCGGAGCCCATTTGTGTAATCACCC 1805
QY 2113 AAAACCCCGGCTGTGCTGTTTCCCTTCTGCGCTACCTTGTAGTAGTTGAGCACTT 2172
Db 1806 AAAACCCCGGCTGTGCTGTTTCCCTTCTGCGCTACCTTGTAGTAGTTGAGCACTT 1865
QY 2173 GATACATCAGACTCATACAAA 2195
Db 1866 GATACATCAGACTCATACAAA 1888

RESULT 4
US-09-148-545-86
; Sequence 86, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; EARLIER FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
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/ EARLIER APPLICATION NUMBER: 60/057,650
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/ EARLIER APPLICATION NUMBER: 60/056,884
/ EARLIER FILING DATE: 1997-08-22
/ NUMBER OF SEQ ID NOS: 280
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 86
/ LENGTH: 1925

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	Query Match	81.2%;	Score 1788.8;	DB 10;	Length 1925;
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				Gaps	2;
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Db	6	AGGAGCTGGCGCTGCAGACTGGGCTTCGGGCCCTGTGCAGAGGAGCAGGCCCTTCCTGAG	65		
QY	406	CAGGAGGAGCAGGTGTGTGGCCGCGCCCTTGAGGCGAGGCCCTGCAGCTGGATGGAGACCT	465		
Db	66	CAGGAGGAGCAGGTGTGTGGCCGCGCCCTTGAGGCGAGGCCCTGCAGCTGGATGGAGACCT	125		
QY	466	GCAGGAGGATGAGATCCGAGTGGTAGCTATTATGCGCACTGGTGTGGGATCGGGCAAT	525		

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3	PRIOR APPLICATION NUMBER: 60/056,889
4	PRIOR FILING DATE: 1997-08-22
5	PRIOR APPLICATION NUMBER: 60/056,893
6	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/056,630
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44	PRIOR FILING DATE: 1997-08-22
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47	PRIOR APPLICATION NUMBER: 60/057,761
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49	PRIOR APPLICATION NUMBER: 60/047,599
50	PRIOR FILING DATE: 1997-05-23
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61	PRIOR APPLICATION NUMBER: 60/047,589
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63	PRIOR APPLICATION NUMBER: 60/047,593
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69	PRIOR APPLICATION NUMBER: 60/043,576
70	PRIOR FILING DATE: 1997-04-11
71	PRIOR APPLICATION NUMBER: 60/047,501
72	PRIOR FILING DATE: 1997-05-23
73	PRIOR APPLICATION NUMBER: 60/043,670

QY 1993 CTT-CAGAGCCTCGGCTCAGGTGGCACTGTCCAGGGTCCAGGCTCAGGCTGGGAGCT 2051
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 Db |||||
 1746 CCCTTGGCCCTCAGCAGTTTGCAGTGGGTAAGGAGGCCAAGCCCATTTGTGTAATCACC 1805
 QY 2112 CAAACCCCGCCCTGTGCCTCTTTTCCCTCTCGGCTACCTTGAGTAGTTGGAGCACT 2171
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 1806 CAAACCCCGCCCTGTGCCTCTTTTCCCTCTCGGCTACCTTGAGTAGTTGGAGCACT 1865
 QY 2172 TGATACATCACAGCACTCATACAA 2195
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RESULT 6

US-09-148-545-21
 ; Sequence 21, Application US/09148545
 ; Publication No. US20030027132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 70 Human Secreted Proteins
 ; CURRENT APPLICATION NUMBER: US/09/148,545
 ; FILE REFERENCE: P2001P1
 ; EARLIER APPLICATION NUMBER: PCT/US98/04482
 ; EARLIER FILING DATE: 1998-09-04
 ; EARLIER FILING DATE: 1998-03-06
 ; EARLIER APPLICATION NUMBER: 60/040,162
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,333
 ; EARLIER FILING DATE: 1997-03-07
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; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 1818

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Best Local Similarity 97.4%; Pred. No. 0;
Matches 1745; Conservative 3; Mismatches 7; Indels 36; Gaps 3;

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QY      510 GTGGGATCGGGCAATGACTTCCCTGTATGGGCAGCTGGCTGGCTGAA--GGAGCTGGG 567
Db      1758 GTGGGATCGGGCAATGACTTCCCTGTATGGGCAGCTGGCTGGCTGAAAGAGCTGGGG 1699

QY      568 CCTCTTGATTCGCTCTCTCATACACCGGGGCTCGGGCTCCACTGGGCTTGGCCAA 827
Db      1698 CCTCTTGATTCGCTCTCTCATACACCGGGGCTCGGGCTCCACTGGGCTTGGCCAA 1639

QY      628 CTTTATGAGGACCCAGAGTGTCTCAGAGAGACCTGGCAGGGCCCACTGAGTTGCTGAA 687
Db      1638 CTTTATGAGGACCCAGAGTGTCTCAGAGAGACCTGGCAGGGCCCACTGAGTTGCTGAA 1579

QY      688 GACCCAGGTGACCAAGCAAGCTGGGTGTGTGGCCCCCAGCCAGCTCAGCGGTACCG 747
Db      1578 GACCCAGGTGACCAAGCAAGCTGGGTGTGTGGCCCCCAGCCAGCTCAGCGGTACCG 1519

QY      748 GCAGGAGCTGGCGAGCGTGCCCGTTGGGCTACCAAGTGTTCACCAACTGTGGGC 807
Db      1518 GCAGGAGCTGGCGAGCGTGCCCGTTGGGCTACCAAGTGTTCACCAACTGTGGGC 1459
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QY	808	CCTCATCAACGAGGCGCTGCTGCATGATGAGCCCATGATCACAAAGCTCTCAGATCAACG	867
DB	1458	CCTCATCAACGAGGCGCTGCTGCATGATGAGCCCATGATCACAAAGCTCTCAGATCAACG	1399
QY	868	GGAGGCGCTGAGTGCATGCGCAGAACCCCTCTGCCATCTACTGTGCGCTCAACACCAAGG	927
DB	1398	GGAGGCGCTGAGTGCATGCGCAGAACCCCTCTGCCATCTACTGTGCGCTCAACACCAAGG	1339
QY	928	GCAGAGCCTGCACCATTTTGGAAATTTGGGAGTGGTGGAGTTCTCTCCCTACGAGGTGCG	987
DB	1338	GCAGAGCCTGCACCATTTTGGAAATTTGGGAGTGGTGGAGTTCTCTCCCTACGAGGTGCG	1279
QY	988	CTTCCCCHAAGTACGGGGGCTTCATCCCTCTGAGCTCTTTGGCTCCGAGTCTTTATGGG	1047
DB	1278	CTTCCCCHAAGTACGGGGGCTTCATCCCTCTGAGCTCTTTGGCTCCGAGTCTTTATGGG	1219
QY	1048	GCAGCTGATGAAGAGGCTTCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAA	1107
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QY	1108	CCTGTATGACGCCAACCTCCAGGACAGCTTATATCTGGGCTCTGAGGCCAGCGATCTCG	1167
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QY	1168	GGACGGCTGGTCAAGAACACAGGCCAACCTGGACAGGACAGGTCCCCCTCTGAAGAT	1227
DB	1098	GGACGGCTGGTCAAGAACACAGGCCAACCTGGACAGGACAGGTCCCCCTCTGAAGAT	1039
QY	1228	AGAAAGAACCCCTCAACAGCGCGCAATAGCTGAGTTTTCACGATCTTCTGACGTG	1287
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QY	1288	GGGTCCACTGGCCGAGGCCACACATAATTTCCCTGGTGGCTCCATTTCCACAAAGACTA	1347
DB	978	GGGTCCACTGGCCGAGGCCACACATAATTTCCCTGGTGGCTCCATTTCCACAAAGACTA	919
QY	1348	CTTTCAGCATCTCACTTCTTCACATGGAAGTACCACTCTGGATGGGCTCCCCAACCA	1407
DB	918	CTTTCAGCATCTCACTTCTTCACATGGAAGTACCACTCTGGATGGGCTCCCCAACCA	859
QY	1408	GCTGCACACCTCGAGGCCACCACTGTCGCTGCGATGTTGGTACTCATCATATACCAG	1467
DB	858	GCTGCACACCTCGAGGCCACCACTGTCGCTGCGATGTTGGTACTCATCATATACCAG	799
QY	1468	CTGCTGCGCCCTCTCGAGCCCACTCGGACGTGGACCTCATCTCTGATTCGACTACAA	1527
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DB	738	CCCTCCAGGAGCCTTCCAGGAGTTCAGCTCTCTGGGCGGGTTCTGCAGGACAGGGGAT	679
QY	1588	CCGGTTCCCAACCCATCTGCCAGCCCCCAAGAGAGAGCTCCAGCTCTGGAGTGCACAC	1647
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QY	1648	CTTCTCCGACCCCACTGTCGCCCGGAGCCCTCGCGTGTGCACTTT-----	1693
DB	618	CTTCTCCGACCCCACTGTCGCCCGGAGCCCTCGCGTGTGCACTTT-----	559
QY	1694	-----TCTCTGGGGTCCGGCGGACAACCCGAGGAGCGGAGCTGG	1734
DB	558	CTCTCTCCGGAGTACTCGGCGCCCTGGGTCCGGCGGACACCCGAGGAGCGGAGCTGG	499
QY	1735	GGAGGTGAACCTGTCTTTCATCGGACTCTCCCTACCACTACAGAGGTGACTCAGCCA	1794
DB	498	GGAGGTGAACCTGTCTTTCATCGGACTCTCCCTACCACTACAGAGGTGACTCAGCCA	439
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DB	438	GGAGGACGTGGACAAGCTGCTGCACCTGCACATTTACAATGTCTGCAACAACAGGAGCA	379
QY	1855	GCTGCTGGAGGCTCTGCGCGCAGGAGTGCAGCGGAGCGGACGCGCGGCCCACTGATG	1914

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; Sequence 87, Application US/09148545
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 1818
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Query Match 76.1%; Score 1676.6; DB 10; Length 1818;
Best Local Similarity 97.4%; Pred. No. 0;
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QY	568	CTCTTTGATTCGCTCTCTACATCACCGGGGCTTCGGGCTCCACCTGGGCTCTTGGCCAA	627
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QY	628	CTTTTATCAGGACCCAGAGTGGTCTCAGAAGAACTTGCAAGGGCCACTGAGTTGCTGAA	687
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Db	1578	GACCCAGGTGACCAAGAACAAAGCTGGGTGCTGTGGCCCCCAGCAGCTGCAGCGGTACCG	1519
QY	748	CGAGAGCTGGCCGAGCGTGCCCGCTTGGGCTACCAAGCTGTCTTACCACACTGTGGGC	807
Db	1518	CGAGAGCTGGCCGAGCGTGCCCGCTTGGGCTACCAAGCTGTCTTACCACACTGTGGGC	1459
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Db	1458	CCTCATCAACGAGGGCTGTGCAATGATGAGCCCCCATGATCAAGCTCTCAGATCAACG	1399
QY	868	GGAGCCCTTGAGTCATGSCCAGAACCTCTGCCCATCTACTGTGCCCTCAACCCAAAGG	927
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QY	1048	GCAGCTGATGAAGAGGCTTCCTGAGTCCCGCATCTGCTTCTTAGAGGTATCTGGAGCAA	1107
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QY	1108	CTGTATGCAAGCAAACCTCAGGACAGCTTATATCTGGGCTCAGAGCCAGCCAGTTCTG	1167
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QY	1168	GGACCGCTGGGTGAGNAACGAGCCAACTGGCAAGAGGAGGTCCTCCCTTCTGAAGAT	1227
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QY	1228	AGAAGAACCAACCTCAACAGCCGGCAGATAGCTGAGTTTTCACCGATCTTCTGACGTG	1287
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QY	1288	GCCTCACTGGGCCAGGCCACAATAAATTTCTGCGTGGCTCCCATTTCCACAAGACTTA	1347
Db	978	GCCTCACTGGGCCAGGCCACAATAAATTTCTGCGTGGCTCCCATTTCCACAAGACTTA	919
QY	1348	CTTTCAGCATCTCACTTCTCCATGAGAAAGCTACCACTCTGGATGGGCTCCCCAAGCA	1407

APPLICANT: LAL, Preeti; RAMKUMAR, Jayalaxmi;
APPLICANT: NGUYEN, Damiel B.; BAUGHN, Mariah R.
TITLE OF INVENTION: LIPID METABOLISM MOLECULES
FILE REFERENCE: PI-0152 USN
CURRENT APPLICATION NUMBER: US/10/332,426
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US 60/216,803
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,801
PRIOR FILING DATE: 2000-07-07
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PRIOR FILING DATE: 2000-07-26
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SOFTWARE: PERL Program
SEQ ID NO 14
LENGTH: 3197
TYPE: DNA
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040029136A1 7477093CB1
US-10-332-426-14

Query Match 27.3%; Score 602; DB 13; Length 3197;
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QY 435 TGAGCAGGCTCCGAGCTGGATGAGACCTCAGAGGATGAGATCCAGCTGGTGGCTA 494
Db 1538 TGAAGCAGCCTTGAGCTGGACAGACCTCAGAGGATGAGATACCCGTTGTGGCA 1597

QY 495 TTATGGCCACTGGTGGTGGATCCGGGCAATGACTTCCCTGTATGGGAGCTGGCTGGCC 554
Db 1598 TCATGGCCACAGAGGAGGTGCCGGGCCATGACCTCACTTACGGCCACCTATTGGCT 1657

QY 555 TGAAGGAGCTGGGCTTCTTGATGGCTCTCTACATACCGGGGCTCGGCTCCACCT 614
Db 1658 TGCAGAGCTGGGCTTCTTAGACTGTGTGACCTTCTAGTGGCTCTCTGGCTTACGT 1717

QY 615 GGCCCTTGCCCAACCTTTATGAGGACCCAGAGTGGTCTCAGAGGACCTGGCAGGCCCA 674
Db 1718 GGAATATGCCACCTGTACGGGACCTGTAGTGGTTCGAGAGGACCTGGAGGACCTA 1777

QY 675 CTGAGTGTCTGAAGACCCAGGTGACCAAGAAAGCTGGGTGTGCTGGCCCCCAGCCAGC 734
Db 1778 TCAGATACGCCCGGAGCAGCTGGCCAGAGAAAGCTGGAGGTCTTTCCCCAGAGCGCC 1837

QY 735 TGCAGCGGTACCGCAGGAGCTGGCCGAGCGTGGGCTACCCAAAGCTGTCTCA 794
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QY 795 CCAACCTGTGGGCTTCATCAACAGGCGCTGTGATGATGAGCCCATGATCAAGC 854
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QY 1155 CCAGCCAGTTCTGGACCGCTGGGTCAAGAACACAGGCCA-----ACC 1196
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QY 1197 TGGACAAAGGAGCAGGCTCCCTTCTGAAATAGAGAACCACTCTCAACAGCCGGAGAA 1256
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QY 1377 AAGCTACCACTCTGATGGGCTCCCAACCAAGCTGACACCTTCGGAGGCCACCTGTGCC 1436
Db 2498 CAGACTACCACTTGACTCCATGCCAGCAGCTGACCCCAAGAGGCCCGGCTCTGCC 2557

QY 1437 TGCTGAGTGGCTTACCTCATCATACAGCTGCTGCCCTCTCTGAGGCCACTCGGG 1496
Db 2558 TGGTGGAGCGGCTTACTTCAACACCAAGCTCTCCCTCATGTTTCGGGCCAGGCCGA 2617

QY 1497 ACGTGGACTCATCTCTGTCATTGGACTACAACCTCCAGGAGCTTCCAGCATGTGACG 1556
Db 2618 GGCTGGAGCTCATCTCTCTCTGACTACTCCCTATCTGCGGCTTTCGAGGCACTGACG 2677

QY 1557 TCCTGGGCGGCTTTCGAGGAGCAGGAGTCCCTTCCCACTCTGCGCCAGCCCG 1616
Db 2678 AGACGAGCTGTACTGCGGGGCTGCCCTTCCCGGGTGGAAACCAAGCCCTC 2737

QY 1617 AAGAGAGCTCCAGCTCGGAGTGCACACCTTCTCGAGCCCACTGCCCCGAGGCC 1676
Db 2738 AGGACAGCAGCAGGCAAGGGAATGCCACCTTTCTCAGACCCGCTGCCCCGAGGCC 2797

QY 1677 CTGCGGTGCTGCATTT-----TTCTCTTGGGG 1703
Db 2798 CGATCTGTGACTTCTCCGCTGGTCAATGCTCTTCAAGGACCACTCAGGCCCGGTG 2857

QY 1704 TCCGGCGGACACCCGAGGAGGCGAGCTGGGAGGAGTGAACCTGTCTTCACTCGGATCTC 1763
Db 2858 TCCAGCGAGCCCGCAGAGCTCCAGGCTGGCGCAAGTGTATCTACCGGGGCGACCTGCC 2917

QY 1764 CTTACCACTACAGAGGTGACCTACAGCCAGGAGGAGCTGGACAGAGCTGTGCACCTGA 1823
Db 2918 CTTACACCTGTCCAAATGACATGACTACAGAGGAGAGCTTCAGAGCCCTGTCTGGGCTCA 2977

QY 1824 CACATTACATGTCTGCAACCAACAGGAGCAGCTGTGGAGGCTGTGGCCAGGAGGTGC 1883
Db 2978 GTGACTACAACTGTGACAGCCAGGAGGAGCTTCTGAGGCTTCTGAGGAGGAGGTGC 1883

QY 1884 AGCGGAGG 1891
Db 3038 AGCACCGG 3045

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US-09-918-995-32564
; Sequence 32564, Application US/09918995
; Publication NO. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20

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RESOLUT IZ
US-10-467-248-10
; Sequence 10, Application US/10467248
; Publication No. US20040086905A1
; GENERAL INFORMATION:
; APPLICANT: DAS, Debopriya; YAO, Monique G.;
; APPLICANT: ARVIZU, Chandra S.; BAUGHN, Mariah R.;
; APPLICANT: LU, Yan; HAFALIA, April J.A.;
; APPLICANT: CHAWLA, Navinder K.; GRIFFIN, Jennifer A.;
; APPLICANT: LU, Dyung Aina M.; YUE, Henry;
; APPLICANT: DING, Li; ELLIOTT, Vicki S.;
; APPLICANT: FORSYTHE, Ian J.; RAMKUMAR, Jayalaxmi;
; APPLICANT: GANDHI, Ameeta R.; TSON, Craig H.;
; APPLICANT: WARREN, Bridget A.; ISANG, V. Tom;
; APPLICANT: EMERLING, Brooke M.; HONCHELL, Cynthia D.;
; APPLICANT: LYNE, Michael; BARROSO, Ines
; TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
; FILE REFERENCE: PI-0358 USN
; CURRENT APPLICATION NUMBER: US/10/467,248
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03813
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/266,910
; PRIOR FILING DATE: 2001-02-06

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PRIOR APPLICATION NUMBER: US 60/276,891
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/276,855
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/279,760
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/283,818
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/285,405
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 3879
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: incyte ID No: 7472774CB1
US-10-467-248-10

Query Match 19.5%; Score 429.6; DB 17; Length 3879;
Best Local Similarity 56.2%; Pred. No. 1.9e-105;
Matches 909; Conservative 0; Mismatches 644; Indels 63; Gaps 3;

Qy 353 CTGGCCGTGCGACGTGGGCTTCGGGCTTCGAGGAGGAGGCGCTTCCTGAGCAGGAGG 412
Db 1681 CTGACGCTGGCGCTGGGCTTCAGGCTGTCGAGGAGGAGGAGGAGGAGGAGGAGG 1740

Qy 413 AAGCAGGTGGTGGCGCGGCTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 472
Db 1741 AAGGTGCTGGTGGCGCGGCTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1800

Qy 473 GATGAGATCCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 532
Db 1801 GACGAGGTGGCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860

Qy 533 CTGTATGGGAGCTGGCTGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 592
Db 1861 ATGTATGGGAGCTGGCTGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920

Qy 593 ACCGGGGCTCGGGCTCCACCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 652
Db 1921 ACTGGTCTATGAGGGGCGACCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 1980

Qy 653 CAGAGGACCTGGGAGGCGGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 712
Db 1981 TCCAAAACTTGGAGCTGCTATCTTTGAGGCTCGGAGGAGGAGGAGGAGGAGGAG 2040

Qy 713 GGTGTGCTGGCGGCGGAGCTGAGCGGTACCGGAGGAGGAGGAGGAGGAGGAGGAGG 772
Db 2041 CCTCCCTGTTCCGAGCAGCTCCGAAATTCAGGAGGAGGAGGAGGAGGAGGAGGAG 2100

Qy 773 TTGGGCTACCCAAAGTGTCTACCAACCTGTGGGCTTCATCAAGAGCGGTGTGTGCAT 832
Db 2101 GAAGGCTACAGGCTACCTTTACAGACTTCTGGGCTGCTGATAGAGACTGCTGGGG 2160

Qy 833 GATGAGCCCCATGATCAAGCTCTCAGATCAAGCGGAGGCGCTGAGTCAATGCGCAGAC 892
Db 2161 GACGAGAGAAATGAATGCAAACTGTGAGTCAAGCTGCTGCTTTGAGCTGGCGCCAGA 2220

Qy 893 CCTCTGCCATCTACTGTGCTCCCTCAACACCAAGGCGAGGCTGACCACTTTTGAATTT 952
Db 2221 CCCCCCTCATCTA-----CCTTACCATCATATGTCAAGATGATGATGACCAAGGAT 2274

Qy 953 GGGGAGTGGTGGAGTGTCTCCCTACGAGGTCGGCTTCCCCAAGTACGGGGCTTCATC 1012
Db 2275 GTGAGTGGTTCAGTGTCTCCCTACGAGTGGGCTTCAGAGGATGATGGGGCTTCATC 2334

Qy 1013 CCTCTGAGCTCTTGGCTCGAGTCTTTATGGGAGCTGATGAGGCTTCTCTGAG 1072
Db 2335 CCTCTGAGCTCTTGGCTCGAGTCTTTATGGGAGCTGATGAGGATTCCTCGAG 2394

Qy 1073 TCCCGCATCTGCTTTAGAGGTATCTGGAGCAACCTGTATGACGCAACCTCCAGGAC 1132
Db 2395 TCTCGAATCTGTACATGCTTAGGCTGTGGAGCAGCATCTTCTCCCTGAACCTGCTGGAT 2454

Qy 1133 AGCTTATCTGGGCTTCAGAGCCAGCAGTTCCTGGGACCGCTGGGTGAGAAACAGGCC 1192
Db 2455 GCTTGAACCTGTTCACACACCTCGGAGGAGTTCCTCCACAGGTGGACAAGGGAGAAAGTG 2514

Qy 1193 AACCTGGACAAGGAGCAGGTCCCTTCTGAAGATGAAGAACCAACCTCAA----- 1244
Db 2515 CAGGACATCGAAGAGCAGGCGATCTGCTGCTGAAATCCCAATGTGATGTAAACATCTG 2574

Qy 1245 -----CAGCGGCGAGATAGTGTAGTTCCTGCGATTTTTCACCGATCTTCTGACG 1285
Db 2575 GAGACACGGTAGTGATCCAGGGTATGCTGTCAAATCTTTTCCGAGAAATCTTTACC 2634

Qy 1286 TGGGTCTCACTGGCCAGGCGCACATAATTTCTGCTGGTGGCTTCCATTTTCCAAAGAC 1345
Db 2635 CATCGTCTTCTGCTGAGTTTCAAACTTCTCTGCTGGCTGCACTGACACCAAC 2694

Qy 1346 TACTTTTCAGCATCTCTTCTCCACATGGAAGTACCACTCTGGATGGGCTCCCAAC 1405
Db 2695 TACCTCCAGAATGGCCAGTTCCTTAGGTGGAAGACACAGTGTAGATGTTTCCCAAC 2754

Qy 1406 CAGCTGACACCTCGGAGCCCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1465
Db 2755 CAGCTGACGAGTCCGGAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2814

Qy 1466 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1525
Db 2815 AGCTACCGGCTTCTCTGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2874

Qy 1526 AACCTCCACGAGGCTTCCAGCAGTGTGAGTGTGCTGGGCGGCTTCTGCGAGGAGGAGG 1585
Db 2875 TGTGCTGGGCTCCAGACAAAGCCCTGAAACAAACCTGTGAGTACTGCACTGTGCGAAG 2934

Qy 1586 ATCCGTTTCCC-----ACCATCTCGCCAGGCCCC 1615
Db 2935 ATCCCTTTCCCAATAACAGCTGCCAGTGAAGATGAAATCTCAAGAAATGTACTCTG 2994

Qy 1616 GAAGAGCAGTTCAGCCTCGGAGTGCCACACCTTCTCCGACCCACCTGCCCCGAGGCC 1675
Db 2995 ATGGAGAACCCCGAGGAGCCGATGCCCATCTGTAATCTTCTCCCACTCATCAATGAC 3054

Qy 1676 CCGTGGTGTGCTGCTTCTTCTGCTGGGTCCGGCGGACACCGAGGAGGCGGAGTGGG 1735
Db 3055 ACTTCCGAAATAACAAGGCAACAGGTGTAGAGCGAAGCCCTGAGGAGGCTGGAGGAGG 3114

Qy 1736 GAGGTGAACCTGCTTCTATCGGACTCTCCCTACCACTACCAAGGTGACCTACAGCCAG 1795
Db 3115 CAGGTGGAATTTATGTTGTTCCCAAACTCCCTATGCGACCAAGAGGCTGACATACAGAG 3174

Qy 1796 GAGGACGTGGACAAGCTGCTGACCTGACATTAATGCTGCTGCAACCAAGGAGGAG 1855
Db 3175 GCCACTTTGACAGCTGTGTGAACCTCTCAGAGTATAACATCTGTAATAATAAGGACAT 3234

Qy 1856 CTGCTGGAGGCTTCTGCGCCAGGAGGCTGAGCGGAGGCGGAGGAGGCGGAGGCGGAG 1911
Db 3235 CTCTCCAGGCTCTGCGGCTCGAGTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3290

RESULT 13
US-10-380-873B-2
; Sequence 2, Application US/10380873B
; Publication No. US20040014089A1
; GENERAL INFORMATION:
; APPLICANT: Hiromasa MIYAJI, et al.
; TITLE OF INVENTION: Polypeptide having phospholipase A2 activity
; FILE REFERENCE: 2139.34
; CURRENT APPLICATION NUMBER: US/10/380,873B
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: JP 00/146466
; PRIOR FILING DATE: 2000-09-19

Query Match	16.6%	Score 365;	DB 16;	Length 2694;
Best Local Similarity	54.3%;	Pred. No. 4.7e-88;		
Matches	882;	Conservative 0;	Mismatches 665;	Indels 78; Gaps 4;
QY	348	GGGAGCTGGCGCTGCGACTGGCTTCGGGCTTCGGGAGGAGCAGGCCTTCTGACGA	407	
Db	968	GGGACTTGGACCTTGGCCCTTGGTTTGACCTCTGTGATGGAGAGCAGGAATTTCTGGACA	1027	
QY	408	GGAGGAACAGAGTGGTGGCCCGCGCCCTTGAGGCAGGCGCTTCGCAGCTGGATGGAGCACTGC	467	
Db	1028	AGAGGAGCAGGTGGCGTCCAGGCCCTGCAGCGGCTGATGGGATTCAGGTGAGGCTCTGC	1087	
QY	468	AGGAGGATGAGATCCCAAGTGGTAGCTATTATGGCCACTGGTGTGGGATCCGGGCAATGA	527	
Db	1088	ACTGTGACCAAGGTACCTGTGTAGCCGTGTAGGCTCTGGGGGTGGAAACAGAGCCATGA	1147	
QY	528	CTTCCCTGTATGGCAGCTGGCTGGCTTGAAGAGCTGGGCTCTTTGGANTGGCTCTCCT	587	
Db	1148	CTTCCCTGTACGGAGCGCTGGCTGGGCTGCAGGAGCTTGGTCTTCTTGGATGCGCTGACCT	1207	
QY	588	ACATCAACCGGGGCTTCGGGCTCCACCTGGGCCCTTGGCCACCTTTATGAGGCCACAGT	647	
Db	1208	ACCTGAGTGGGCTCTCTGGTCTTCTTGGTGCACTCTACACTCTAAGGGATCCATCCT	1267	
QY	648	GGTCTCAGAGGACCTGGCGAGGGCCCACTGAGTTGCTGGAAGACCCAGGTGACCAAGACA	707	
Db	1268	GGTCCACAGAGGCTTTGCAAGGGCCCCATTAAATATGCCTCAGAGCGAGTCTGCAGCACTA	1327	
QY	708	AGCTGGGTGTGCTGGCCCCCGCCAGCCAGCTGAGCGGTACCGGACAGAGCTGGCGAGCGTG	767	
Db	1328	AAATTGGGATGCTGTCTCCCAAGCAGTTTGAATACTACTCCCGGAAAAAGAGCGCTGGG	1387	
QY	768	CCCGTCTGGGCTACCCAAGCTGTCTCACCAACTGTGGGCCCTCATCAACGAGGCGCTGC	827	
Db	1388	AGAGCAGGGGACACAGCATGTCTTTCACCTGACTTGTGGGCTCTCATCATGTAGTATTTCC	1447	
QY	828	TGCATGATGAGCCCCATGATCAAGCTCTAGATCAACGGGAGGCGCTGAGTCAATGGCC	887	
Db	1448	TGAACCCAGAGGAAAAACCTGCCAAGTGTGACACGACGAAAGGTCAGCCAGGGTC	1507	
QY	888	AGAAACCTCTGCCCATCTACTGTGGCTCAACACCAAGGGCAGAGCCTGACCACTTTTG	947	
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QY	948	AAATTTGGGAGTGGTGGAGTTCTCTCCCTACGAGTGGCTTCCCAAGTACGGGGCT	1007	
Db	1565	ACTTTTCAGAGTGGTGGAGTTCACCCCCTATGAGGTGGTTTCCCCAAGTACGGGGCTT	1624	
QY	1008	TCATCCCTCTGAGCTCTTTGGCTCCGAGTCTTTTATGGGGCAGCTGATGAAGAGCTTC	1067	
Db	1625	ACGTTTCCCAACGAACTCTTTGGCTCTGAATCTTTCATGGCCGGCTGTGATTTCTGGC	1684	
QY	1068	CTGAGTCCCGATCTGCTTCTTAGAAGGTATCTGAGCAACCTGTGATGACGCCAACCTCC	1127	
Db	1685	CAGAGCCCCGATCTGTTTACCTGCAAGGTATGTGGGGAAGTGCTTTTTCAGCCAGCCCTGT	1744	
QY	1128	AGGACAGCTTACTTGGGCGCTCAGAGCCAGCCAGTCTTGGGACCGCTGGGTGAGGAACC	1187	
Db	1745	ATGAGATCTTCTGAGCTGGAGGCGCTTAGCGCTGAGCTTTCTGCACTGGCACAGGGGGA	1804	

QY	1188	AGGCCAACTGACAA-----GGAGCAGGTCCCCCTTCTGAAGATAG	1229
Db	1805	GTGTCAGTGTACACATGACTGGCCAAAGTTACGGAAGCAGAGCCACACAGCGTGCCTA	1864
QY	1230	AGAAACCACCTTCACACCGCGCAGAATAGTGTAGTGTTTTTCACCGATCTTCTGACGTGGC	1289
Db	1855	CGAGACTCTTCAGCGCAATGAGTTCCTTCTCTCAGGCTGTCTGGACATATTCACCTCCC	1924
QY	1290	GTCCAGTGGCCCGAGGCCACACATAATTTCTGCGTGGCCCTCCATTTCCACAAGACTACT	1349
Db	1925	GTATTACTTGTGGCCAGACCTTTAACTTTACCCGAGGTCTCTGATGTACAAAGACTACA	1984
QY	1350	TTACGATCTCACTTCTTCCACATGGAAGCTAC-----CACTC	1388
Db	1985	CAGCTAGAAAGGACTTCGTGTCTCTGAAGATGATGGCATTCACATACTATGGATACC	2044
QY	1389	TGGATGGCTCCCCAAACAGCTACACCTTCGAGCGCCACACCTGTGCTGCTGGATGTTG	1448
Db	2045	CTGATGCTGTCCCAACAGCTCACCCATGAAGGACTTCCTGTCTCCCTAGTAGATGGAG	2104
QY	1449	GCTACCTCATCAATPACAGCTGCTGCCCTCCTCGAGCCCACTCCGGAGCTGGEACTCA	1508
Db	2105	GCCTTGTATCAACTCGCCATTTCCACTGGTCTCTGACGGCAGCGGCTGTGGACCTCA	2164
QY	1509	TCCTGTCAATTTGGACTACAACTCCAGGAGCCTTCAGCAGTTTGACAGTCTCTGGGCCGT	1568
Db	2165	TTGTGTCCTTTGACTATTCTCTGGAAAGGCCCTTTTGAGGTCTCTGACAGTGACAGAGAGT	2224
QY	1569	TCTGCCAGGACAGGGGATCCCTCTCCACCCCATCTCGCCCCAGCCCCGAGACGACTCC	1628
Db	2225	ACTGCCGGACCGAGGATCCCTTCCCAAGATTGAGTGGAGCCCCAAGGACTCTGAAG	2284
QY	1629	AGCTCGGAGTGCACACCTTCTCCGACCCCACTTGCCTCCCGAGCCCTCGCGTGCTGC	1688
Db	2285	ACCCCCGTGAATCTATCTGTGTGTCGAGCAGAGGACCCCTGCTCGCCCATCGTGCTGC	2344
QY	1689	ACTTTTCTCTCTGG-----GGTCCGGGGGA	1712
Db	2345	ATTTCCTCTTGTCAACAGACCTTTCGACGCACTGGCCCCAGTGTGGAAACACAAA	2404
QY	1713	CACCGAGGAGCGGAGCTGGGGAGGTGAACCTGTCTTCATCGGACTCTCCCTACCCT	1772
Db	2405	CAGCTGAGGAGAAGGCCTTCGGGGACTTATCATCAACGGGCCAGATCTGCCTATGGCA	2464
QY	1773	ACAGAAAGTGCCTACAGCCAGGAGGAGCTGGCAAGTGTGTGCACTTGACACATTACA	1832
Db	2465	TGATGATTTCCTACGAGGCCCAAGGAATTTGATCGGCTGGTGACCCCTGAGCCGATACA	2524
QY	1833	ATGTCTGCAACAACAGGAGCAGCTGCTGGAGGCTCTGGCCAGGCACTGCAGCGGAGGC	1892
Db	2525	ACGTCTTGAAACAACAAGGAGACTATACGGCATGCCCTCCAGCTGGCTCTGGACCGGGCGC	2584
QY	1893	GGCAG	1897
Db	2585	GGCAG	2589

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Result	Score	Query Match	Length	DB	ID	Description
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2	892.8	40.5	1131	12	BM928260	AGSCOURT
3	897	31.6	957	14	CA488226	AGCENT
4	677.6	30.7	949	12	BI768993	603058145

REFERENCE AUTHORS	3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861
TITLE	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 4240) Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://phantom.gsc.riken.go.jp/.
FEATURES	source 1..4240 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:A030011C02" /db_xref="MGI:2401694" /db_xref="taxon:10090" /clone="A030011C02" /tissue_type="skin" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="6 days neonate"
misc_feature	1..4240 /note="similar to CYTOSOLIC PHOSPHOLIPASE A2 BETA [Homo sapiens] (SPR 095712, evidence: FASTY, 70.9%ID, 76.7%length, match=2694)"
ORIGIN	Query Match 51.3%; Score 1129.8; DB 11; Length 4240; Best Local Similarity 82.5%; Pred. No. 1.3e-215;
Matches 1321; Conservative 0; Mismatches 247; Indels 33; Gaps 1;	
334	GGATTACAGACTGAGGAGCTGGCCCTGGCGACTGGGCTTTCGGCCCTTTCGGAGAGGACA 393
2270	GGAGNAGACCAAGAGCTGGCTGTGGGCTGGGCTGTGGGCTTTCGGAGGAGCA 2329
394	GGCTTTCCTGAGCAGAGGAGAGAGTGGTGGCGGGCTTTCGGAGGAGGCGCTTCAGCT 453
2330	GGCTTTCCTAAGCAAGAGGAGGAGTGGTGGCGGGCTTTCGGAGGAGGCGCTTTCAGCT 2389
454	GGATGAGAGCTTCAGGAGGAGTCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 513
2390	GGACCAAGAGCTTCAGGAGGAGTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2449
514	GATCCGGGCAATGACTTCCCTGTATGGGAGCTGGTGGCTGAAAGAGCTGGGCTTCT 573
2450	GATCCGGGCAATGACTTCTTTGTATGGGAGCTGGCGGCTTCAGGAGCTTCGCGCTTCT 2509
574	GGATTGGCTTCTTACATACCCGGGCTTCAGAGGAGCTGGGAGGAGCTGGGAGCTTCA 633
2510	CGACTGCATCTCTTATATCAGGGGGCTTCAGGATCCACTGGGCACTGGCCAACTCTTA 2569
634	TGAGGAGGAGGAGTGGTCTCAGAGGAGCTGGGAGGAGGAGCTGGGAGGAGCTTGAAGCCCA 693
2570	TGAGGAGGAGGAGTGGTGGCAGAGGAGCTGGGAGGAGCTGGGAGGAGCTTGAAGCACA 2629
694	GGTGACCAAGAACTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 753
2630	GGTGACCAAGAGGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2689
754	GCTGGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 813
2690	GCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2749
814	CAAGAGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 873
2750	TAATGAGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2809
874	CCTGAGTGCATGGCAGAGGAGCTTCTGCGCATCTGTCCTTCAACCAAGAGGAGGAG 933
2810	CCTGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2869
934	CCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 993
2870	CCTGAGTGCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2929
994	CAAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1053
2930	CAAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2989
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2990	GATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3049
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1174	CTGGGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1233
3110	CTGGGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3169
1234	ACCACCTCAACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1293
3170	GCCACCGACATGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3229
1294	ACTGGGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1353
3230	CCTGGGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3289
1354	GCATCTCTCTCTCCACATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1413
3290	GAACTCTCTCTCTCCACATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3349

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH MGC Library."

Query Match	40.5%;	Score 892.8;	DB 12;	Length 1131;
Best Local Similarity	93.4%;	Pred. No. 3.8e-168;		
Matches 998;	Conservative 0;	Mismatches 60;	Indels 11;	Gaps 6;
QY	627	ACCTTTATGAGGACCCACAGTGGTCTCAGAAGAGCACTGGCAGGGCCACCTGAGTTCTCTGA	686	
Db	18	ATCTTTATGAGACCCAGAGTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGA	77	
QY	687	AGACCCAGGTGACCAAGAAACAAGCTGGGTGTGTGGCCCGCCACGACGCTGCAGCGGTACC	746	
Db	78	AGACCCAGGTGACCAAGAAACAAGCTGGGTGTGTGGCCCGCCACGACGCTGCAGCGGTACC	137	
QY	747	GGCAGGAGCTGGCGAGCGGTGGCCCGCTTGGGCTACCCAACTGCTTCACCAACTGTGGG	806	
Db	138	GGCAGGAGCTGGCGAGCGGTGGCCCGCTTGGGCTACCCAACTGCTTCACCAACTGTGGG	197	
QY	807	CCCTCATCAAGAGCGCGTGTGCATCATAGAGCCCATGATCAAGAGTCTCAGATCAAC	866	
Db	198	CCCTCATCAAGAGCGCGTGTGCATCATAGAGCCCATGATCAAGAGTCTCAGATCAAC	257	
QY	867	GGGAGGCCCTGAGTCATGGCCAGAACCCCTCTGCCCATCTACTGTGCCCTCAACACCAAG	926	
Db	258	GGGAGGCCCTGAGTCATGGCCAGAACCCCTCTGCCCATCTACTGTGCCCTCAACACCAAG	317	
QY	927	GGCAGAGCTGACCACTTTTGAATTTGGGAGTGGTGGAGTTCTCTCCCTACGAGGTGCG	986	
Db	318	GGCAGAGCTGACCACTTTTGAATTTGGGAGTGGTGGAGTTCTCTCCCTACGAGGTGCG	377	
QY	987	GCTTCCCAAGTACGGGCGCTTCATCCCTCTGAGCTCTTTGGCTCCGAGTCTTTTATGG	1046	
Db	378	GCTTCCCAAGTACGGGCGCTTCATCCCTCTGAGCTCTTTGGCTCCGAGTCTTTTATGG	437	
QY	1047	GGCAGCTGATGAAGAGGCTTCTGAGTCCCGCATCTGCTTCTTAGAAGTATCTGGAGCA	1106	
Db	438	GGCAGCTGATGAAGAGGCTTCTGAGTCCCGCATCTGCTTCTTAGAAGTATCTGGAGCA	497	
QY	1107	ACCTGTATGAGCAACACTCTCAGGACAGCTTATATGGGCTTCAGAGCCCAAGCAGTTCT	1166	
Db	498	ACCTGTATGAGCAACACTCTCAGGACAGCTTATATGGGCTTCAGAGCCCAAGCAGTTCT	557	
QY	1167	GGGACCGCTGGGTACGAAACAGGCCCACCTGGACAAAGGACAGGTCCCCCTCTGAAGA	1226	
Db	558	GGGACCGCTGGGTACGAAACAGGCCCACCTGGACAAAGGACAGGTCCCCCTCTGAAGA	617	
QY	1227	TAGAAGAACACCTCAACAGCGCGGCAATAGCTGAGTTTTCACCGATCTTCTGAGT	1286	
Db	618	TAGAAGAACACCTCAACAGCGCGGCAATAGCTGAGTTTTCACCGATCTTCTGAGT	677	
QY	1287	GGCGTCCACTGGCCAGGCCACACATATTTCTGCGTGGCTCCATTTCCACAAGACT	1346	
Db	678	GGCGTCCACTGGCCAGGCCACACATATTTCTGCGTGGCGCTCAITTTCCACAAGACT	737	
QY	1347	ACTTTCAGCATCCTCACTTCTCCATGGAAGCTACCACTCTGAGTGGGTCCCCAAC	1406	
Db	738	ACTTTCAGCATCCTCACTTCTCCATGGAAGCTACCACTCTGAGTGGGTCCCCAAC	797	
QY	1407	AGCTGACACCTTCGGAGGCCCACTGTGCCCTGGATGTTGGTACTCATCAATACCA	1466	
Db	798	AGCTGACACCTTCGGAGGCCCACTGTGCCCTGGATGTTGGTACTCATCAATACCA	857	
QY	1467	GCTGCTGCCCTCTCTGACGCCCACTCGGACGTGGAC--TCACTCTGTCAATGGACTAC	1525	

RESULT 2
 LOCUS BM928260
 DEFINITION linear EST 12-MAR-2002
 AGENCOURT_6699873 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770097
 5', mRNA sequence.
 BM928260
 BM928260.1 GI:19378639
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1131)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM12832 row: j column: 18
 High quality sequence stop: 629.
 Location/Qualifiers
 1..1131
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:5770097"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 121"

FEATURES
source

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Db      858  GTGCGTGGCCCTCTCCGAGCCACATCGGAGCTGACCTTATCTGNCAATTTGGACTAC 917
QY      1526  AACCTCCAGGAGCCTTCCAGCAGTTGCGACT--CTGGGCGCGTTTC--TGCCAGAGACA 1581
Db      918  AACCTTCACGGAACCTTCCAGCAGTTGCGACTTCTTGGGCGCGTTCTCTGCCCCGAGCC 977
QY      1582  GGGGA--TCCGTTTCCACCATCTCG-CCAGCCCGAGAGCAGCTCCAGCCTC--G 1635
Db      978  GGGGAATCCGTTTCCACCATTTCCGCCAGCCCAAGAGCGGTTTTCGGCCCTGGG 1037
QY      1636  CGAGTCCCAACCTTCTCCGACCCCACTCCGCCGAGCCCTTCGCGTG 1684
Db      1038  GAAGGCCCAACCCCTTTTGGACCCACTGCGCCCGGAAACCCCTGGG 1086

RESULT 3
CA488226 575 bp mRNA linear EST 14-NOV-2002
LOCUS AGENCOURT_10807975 MAPcL Homo sapiens cDNA clone IMAGE:6719969 5',
DEFINITION mRNA sequence.
ACCESSION CA488226
VERSION CA488226.1 GI:24949530
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Invitrogen Corp
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14278 row: 1 column: 17
High quality sequence stop: 611.
FEATURES
Location/Qualifiers
1..957
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6719969"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
hTERT-HME1, LNCaP"
/lab_host="EMDH10B"
/clone_lib="MAPcL"
/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
Insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkok Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
ORIGIN
Query Match 31.6%; Score 697; DB 14; Length 957;
Best Local Similarity 96.5%; Pred. No. 5.9e-129;
Matches 723; Conservative 0; Mismatches 25; Indels 1; Gaps 1;
QY 342 GACTGAGGAGCTGGCGCTTCCGAGCTTCCGCGCTTCCGAGGAGCAGGCGCTTCC 401
Db 91 GACTGAGGAGCTGGCGCTTCCGAGCTTCCGCGCTTCCGAGGAGCAGGCGCTTCC 150
QY 402 TGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 461

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Db      151  TGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 210
QY      462  ACTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 521
Db      211  ACTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 270
QY      522  CAAATGATTCCTCCCTGATATGGGAGCTGGCTGGCTGAAGGAGCTGGGCTCTTCGATTCG 581
Db      271  CAAATGATTCCTCCCTGATATGGGAGCTGGCTGGCTGAAGGAGCTGGGCTCTTCGATTCG 330
QY      582  TCTCTTACATACCGGGGCTCGGGCTCCACCTTGGGCTTGGGCTTGGGCTTGGGCTTGG 641
Db      331  TCTCTTACATACCGGGGCTCGGGCTCCACCTTGGGCTTGGGCTTGGGCTTGGGCTTGG 390
QY      642  CAGAGTGGTCTCAGAAAGGAGCTCGAGGGGCTCAGTGGTCTGAGTGGTCTGAGAGCAGGAGTGA 701
Db      391  CAGAGTGGTCTCAGAAAGGAGCTCGAGGGGCTCAGTGGTCTGAGTGGTCTGAGAGCAGGAGTGA 450
QY      702  AGAACAGAGCTGGTGGTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 761
Db      451  AGAACAGAGCTGGTGGTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 510
QY      762  AGCGTGGCTGGTGGGCTACCAAGCTGCTTCCAACTTGGGCTTGGGCTTGGGCTTGGGCTTGG 821
Db      511  AGCGTGGCTGGTGGGCTACCAAGCTGCTTCCAACTTGGGCTTGGGCTTGGGCTTGGGCTTGG 570
QY      822  CGCTGCTGCATGATGAGCCCATGATCAAGCTCTCAGATCAACAGGAGGAGGAGGAGGAGTGC 881
Db      571  CGCTGCTGCATGATGAGCCCATGATCAAGCTCTCAGATCAACAGGAGGAGGAGGAGGAGTGC 630
QY      882  ATGCCAGAGACCTTCTGCCATCTACTGTGCTTCAACCAACCAACCAACCAACCAACCAACCA 941
Db      631  ATGCCAGAGACCTTCTGCCATCTACTGTGCTTCAACCAACCAACCAACCAACCAACCAACCA 690
QY      942  CTTTGTGAATTTGGGAGTGGTGGCTGCTCTCTCCCTAGAGGCTGGCTTCCCAAGTACG 1001
Db      691  CTTTGTGAATTTGGGAGTGGTGGCTGCTCTCTCCCTAGAGGCTGGCTTCCCAAGTACG 750
QY      1002  GGGCTTCTATCCCTCTGAGCTCTTGGCTCCGAGTTC-TTATGGGAGCAGTATGAAG 1060
Db      751  GGGCTTCTCTCCCTCTGAGCTCTTGGCTCCGAGTTC-TTATGGGAGCAGTATGAAG 810
QY      1061  AGGCTTCTGAGTCCCGCATCTGCTCTT 1089
Db      811  AAGGCTTCTGAGTCCCGCATCTGCTCTT 839

RESULT 4
BI768993 949 bp mRNA linear EST 25-SEP-2001
LOCUS 603058145F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207531 5',
DEFINITION mRNA sequence.
ACCESSION BI768993
VERSION BI768993.1 GI:15760571
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1520 row: j column: 12

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High quality sequence stop: 900.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5207531"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 122"
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 30.7%; Score 677.6; DB 12; Length 949;
 Best Local Similarity 90.4%; Pred. No. 4.5e-125;
 Matches 850; Conservative 0; Mismatches 44; Indels 46; Gaps 10;

QY 1024 CTTTGGCTCCGAGTTCTTTATGGGCGAGCTGATGAAGGCTTCTGAGTCCCGCATCTG 1083
 DB |||||
 QY 1084 CTTCTTAGAGGTATCTGGAGCAACTGTATGACGCAACTCTCCAGGACAGTTTACTG 1143
 DB |||||
 QY 61 CTTCTTAGAGGTATCTGGAGCAACTGTATGACGCAACTCTCCAGGACAGTTTACTG 120
 DB |||||
 QY 1144 GGCCTCAGAGCCAGCCAGTTCTGGGACCGCTGGGTGAGGACGAGCCCACTGGACAA 1203
 DB |||||
 QY 121 GGCCTCAGAGCCAGCCAGTTCTGGGACCGCTGGGTGAGGACGAGCCCACTGGACAA 180
 DB |||||
 QY 1204 GGAGAGTCCCTCTTGAAGATAGAGAACACCTCTCAAGCCGCGAGATAGCTGA 1263
 DB |||||
 QY 181 GGAGAGTCCCTCTTGAAGATAGAGAACACCTCTCAAGCCGCGAGATAGCTGA 240
 DB |||||
 QY 1264 GTTTTTCACCATCTTCTGAGTGCGGTCCACTGGCCCGGAGCCACACATATTTCTCGG 1323
 DB |||||
 QY 241 GTTTTTCACCATCTTCTGAGTGCGGTCCACTGGCCCGGAGCCACACATATTTCTCGG 300
 DB |||||
 QY 1324 TGGCTCCTCATTTCCACAAAGACTACTTTTCAGATCTCTCACTTCTCCACATGGAAAGCTAC 1383
 DB |||||
 QY 301 TGGCTCCTCATTTCCACAAAGACTACTTTTCAGATCTCTCACTTCTCCACATGGAAAGCTAC 360
 DB |||||
 QY 1384 CACTCTGATGGGTCCGCAACAGCTGACACCTCTGGAGCCCACTGTGCTGCTGGA 1443
 DB |||||
 QY 361 CACTCTGATGGGTCCGCAACAGCTGACACCTCTGGAGCCCACTGTGCTGCTGGA 420
 DB |||||
 QY 1444 TGTGGTCTACTCATCATATACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 1503
 DB |||||
 QY 421 TGTGGTCTACTCATCATATACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 480
 DB |||||
 QY 1504 CCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 1563
 DB |||||
 QY 481 CCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 540
 DB |||||
 QY 1564 CCGTCTTCCGAGGAGGAGGATCCGCTTCCACCCATCTCGCCGAGCCGAGGAGCA 1623
 DB |||||
 QY 541 CCGTCTTCCGAGGAGGAGGATCCGCTTCCACCCATCTCGCCGAG-CCGAGAGCA 599
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 QY 1624 GCTCCAGCTC-GGAGTGCCACACTTCTCGGACCCCACTGCTCCGAGCCCTCGG 1682
 DB |||||
 QY 600 GCTCCAGCTC-GGAGTGCCACACTTCTCGGACCCCACTGCTCCGAGCCCTCGG 659
 DB |||||
 QY 1683 TGCTGCACTTTTC-----CTCTGGGTCCGGCG 1710
 DB |||||
 QY 660 TGCTGCACTTTCTCTGTCAGCGACTCTCTCCGGAGTACTCGGCCCTCGGGTCCGGCG 719
 DB |||||

QY 1711 GACA-CCGAGGAGCGGCGAGCTGGGAGGTGAACCTGT--CTTCATCGACTCTCCCTA 1767
 DB |||||
 QY 720 GACACCCCGAGGAGCGGCGAGCTGGGAGGTGAACCTGTCTTCCATCGACTCTCCCTA 779
 DB |||||
 QY 1768 CCACCTACACG-AGGTGACCTACAGCCAGGAG--ACGTGGACAAGCTGCTGCACCTGA 1823
 DB |||||
 QY 780 CCACCTACACGAATGTGACTTACAGCAGGAGGACCGTGGACCAAGCTGTGCACCTGAA 839
 DB |||||
 QY 1824 CACATTACAAATGTCTGCAACACCAAGGAGCAGCTGTGGAGGCTCTGCGCCAGGCACTGC 1883
 DB |||||
 QY 840 CACATTACAAATGTCTGCAAAACCA-GAGCAAGTGTCTTAAGGCTCTG-GCCAGGCACTGC 897
 DB |||||
 QY 1884 AGCGAGGCGGAGCGGAGCCGAGCCCTGATGATGCGCGGGCC 1923
 DB |||||
 QY 898 AGGGAAGCGGAACGC---AGGCCCTTGTATGGCGCGGCC 934
 DB |||||

RESULT 5
 BU688449/c

LOCUS
 DEFINITION 759 bp mRNA linear EST 07-OCT-2002
 UI-CF-EC1-aea-j-17-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
 UI-CF-EC1-aea-j-17-0-UI 3', mRNA sequence.
 ACCESSION BU688449
 VERSION BU688449.1 GI:23545244
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 759)
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

Location/Qualifiers
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 /db_xref="taxon:9606"
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 /tissue_type="Lung"
 /dev_stage="Adult and Fetal"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-EC1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-EC1 is a normalized cDNA library containing the
 following tissue(s): Normal lung from adult and from fetal
 day 64, day 87, week 19 and week 42. The library was
 constructed according to Ronaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT7T3-Pac vector. The oligonucleotide used to prime

FEATURES
 source

the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGTCTTAC.
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG LIB=UI-CF-EC1
TAG_SEQ=AAGTGTCTTAC"

ORIGIN

Query Match 30.0%; Score 661.4; DB 13; Length 759;
Best Local Similarity 94.2%; Pred. No. 7.9e-122;
Matches 711; Conservative 0; Mismatches 11; Indels 33; Gaps 1;
QY 1483 GCAGCCCACTCGGACCTGACCTCCTGTCATTGGACTACAACTCCACGAGCCTT 1542
DB 759 GCAGCCCACTCGGACCTGACCTCCTGTCATTGGACTACAACTCCACGAGCCTT 700
QY 1543 CCAGCACTTCAGCTCTGGGCGGTTCGCGAGCAGGGATCCGTTCCACCCAT 1602
DB 699 CCAGCACTTCAGCTCTGGGCGGTTCGCGAGCAGGGATCCGTTCCACCCAT 640
QY 1603 CTGCCCCAGCCCCGAGCAGCTCCAGCTTCGGAGTGCACACCTTCTCCGACCCAC 1662
DB 639 CTGCCCCAGCCCCGAGCAGCTCCAGCTTCGGAGTGCACACCTTCTCCGACCCAC 580
QY 1663 CTGCCCCAGCCCCCTGGGCTGCTGCACTTT----- 1693
DB 579 CTGCCCCAGCCCCCTGGGCTGCTGCACTTTCTCTGCTCAGCGACTCTTCCGGGAGTA 520
QY 1694 ----TCTCTCGGGTTCGGGCGGACACCGAGGCGGCGCAGCTGGGAGGTGAACCTGTC 1749
DB 519 CTGCGCCCCCTGGGCTTCGGGAGACACCCGAGAGGCGCAGCTGGGAGGTGAACCTGTC 460
QY 1750 TTCACTCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTTGGACAA 1809
DB 459 TTCACTCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTTGGACAA 400
QY 1810 GCTGCTGACCTGACACATTACATGCTGCAACACAGCAGGAGCTGCTGGAGGCTCT 1869
DB 399 GCTGCTGACCTGACACATTACATGCTGCAACACAGCAGGAGCTGCTGGAGGCTCT 340
QY 1870 GCGCAGCAGTGACGAGCGGCGCAGCGAGGCGCCCACTGATGGCGGGGCGCCCTGCC 1929
DB 339 GCGCAGCAGTGACGAGCGGCGCAGCGAGGCGCCCACTGATGGCGGGGCGCCCTGCC 280
QY 1930 ACCCTTAACCTCTCAATTCCTCCCTGCTGCTGAGTTGACAGTGGGAACTGTATCAGCA 1989
DB 279 ACCCTTAACCTCTCAATTCCTCCCTGCTGCTGAGTTGACAGTGGGAACTGTATCAGCA 220
QY 1990 GTGCTTCAGAGCTCGGGCTCAGGTGGCACTGTCCTCCAGGCTCAGGCTGAGGGCTGGAG 2049
DB 219 GTGCTTCAGAGCTCGGGCTCAGGTGGCACTGTCCTCCAGGCTCAGGCTGAGGGCTGGAG 160
QY 2050 CTCCTCTGCGCTCAGCAGTTTTCAGTGGGGTAAGGAGGCCAAGCCCACTTGTGTAATCA 2109
DB 159 CTCCTCTGCGCTCAGCAGTTTTCAGTGGGGTAAGGAGGCCAAGCCCACTTGTGTAATCA 100
QY 2110 CCAAAAACCCCGGCTCTGCTGTTTCCCTTCTGCTGCTACCTTGTAGTTGAGCA 2169
DB 99 CCAAAAACCCCGGCTCTGCTGTTTCCCTTCTGCTGCTACCTTGTAGTTGAGCA 40
QY 2170 CTTGATACATCAGACTCATACAAAAA 2204
DB 39 CTTGATACATCAGACTCATACAAAAA 5

RESULT 6

BM718675
LOCUS
DEFINITION
UI-E-EO1-ajc-i-21-0-UI r1 UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-ajc-i-21-0-UI 5', mRNA sequence.
ACCESSION
BM718675

VERSION

KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS
TITLE

JOURNAL

MEDLINE
PUBMED
COMMENT

BM718675.1 GI:19037020

EST.
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 647)

Bonaldi,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

1..647

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-E-EO1-ajc-i-21-0-UI"

/tissue_type="fetal eye"

/dev_stage="fetal"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-EO1"

/note="Organ: eye; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EO1 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p773-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGCGTATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI)."

ORIGIN

Query Match 28.7%; Score 633.2; DB 12; Length 647;
Best Local Similarity 99.4%; Pred. No. 3.5e-116;
Matches 635; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 470 GAGGATGAGATCCCAGTGGTACCTTATGGCCACTGTGTGGTGGATCCGGCAATGACT 529
DB 1 GAGGATGAGATCCCAGTGGTACCTTATGGCCACTGTGTGGTGGATCCGGCAATGACT 60
QY 530 TCCCTGTATGGCAGCTGGCTGCTGAAGAGAGCTGGGCTCTTGGATTCGCTCTCTAC 589
DB 61 TCCCTGTATGGCAGCTGGCTGCTGAAGAGAGCTGGGCTCTTGGATTCGCTCTCTAC 120
QY 590 ATCAGCGGGCTCGGGCTCCACCTGGGCTTGGCCAACTTTATCAGCACCAGAGTGG 649
DB 121 ATCAGCGGGCTCGGGCTCCACCTGGGCTTGGCCAACTTTATCAGCACCAGAGTGG 180
QY 650 TCTCAGAAGACCTGGCAGGCGCCACTGATGTTCTCTGAAGACCCAGGTGACCAAGAACAG 709


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Db      41  CACTGTATACATCAGAGACTATACAAAAA 5
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CD252554      869 bp      mRNA      linear      EST 22-MAY-2003
AGENCOURT 14161855 NIH_MGC_181 Homo sapiens cDNA clone
IMAGE:30374934 5', mRNA sequence.
CD252554
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 869)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: ND4W435 row: c column: 07
High quality sequence start: 6
High quality sequence stop: 549.
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/clone="IMAGE:30374934"
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/dev_status="Unknown"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_181"
/note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV
(destroyed); Library is oligo-dr primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 27.6%; Score 608; DB 14; Length 869;
Best Local Similarity 99.0%; Pred. No. 3.8e-111;
Matches 622; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 879 GTCTGTCGACAGACCTCTGCCACTACTGTGCTCAACACCAAGGCGAGCCTCA 938
Db 5 GTCTGTCGACAGACCTCTGCCCTCTCAACACCAAGGCGAGCCTCA 63
QY 939 CCACCTTTTGAATTTGGGAGTGTGGAGTTCTCTCCCTACGAGTGTGGCTTCCCAAGT 998
Db 64 CCACCTTTTGAATTTGGGAGTGTGGAGTTCTCTCCCTACGAGTGTGGCTTCCCAAGT 123
QY 999 AGGGGCTTATCCCTCTGAGCTTTGGCTCCGAGTTCTTATGGGCGAGCTGATCA 1058
Db 124 ACGGGGCTTATCCCTCTGAGCTTTGGCTCCGAGTTCTTATGGGCGAGCTGATCA 183
QY 1059 AGAGGCTTCTGAGTCCGAGTCTGCTTCTTGAAGTATCTGAGCAACCTGTATGCGAG 1118
Db 184 AGAGGCTTCTGAGTCCGAGTCTGCTTCTTGAAGTATCTGAGCAACCTGTATGCGAG 243
QY 1119 CCAACCTCCAGGACAGCTTATCTAGTGGCTCAGAGCCCGAGCTTCTGGGACCGCTGGG 1178
|||||
244 CCAACCTCCAGGACAGCTTATCTAGTGGCTCAGAGCCCGAGCTTCTGGACCGCTGGG 303
|||||
1179 TCAGGAACAGGCAACCTCGCAAGAGCAGGTGCCCTTCTGAAGATAGAAGAACAC 1238
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304 TCAGGAACAGGCAACCTCGCAAGAGCAGGTGCCCTTCTGAAGATAGAAGAACAC 363
|||||
1239 CCTCAACAGCGCGCAGATAGCTGAGTTTTTTCACCGATCTTCTGACGTGGCTCCATGG 1298
|||||
364 CCTCAACAGCGCGCAGATAGCTGAGTTTTTTCACCGATCTTCTGACGTGGCTCCATGG 423
|||||
1299 CCAGGCGCACATATTTTCTCGTGGCTCCATTTCCACAAGAGACTACTTTTCAGCATC 1358
|||||
424 CCAGGCGCACATATTTTCTCGTGGCTCCATTTCCACAAGAGACTACTTTTCAGCATC 483
|||||
1359 CTCACTTCTCACATGGAAGCTACCACTCTGGATGGCTCCCAACAGCTGACACCT 1418
|||||
484 CTCACTTCTCACATGGAAGCTACCACTCTGGATGGCTCCCAACAGCTGACACCT 543
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1419 CGAGGCGCGCAGTGTGCTGATGTGGTACCTCACTCAATACAGCTGCTGCTGCC 1478
|||||
544 CGAGGCGCGCAGTGTGCTGATGTGGTACCTCACTCAATACAGCTGCTGCTGCC 603
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1479 TCCTGCGAGCCCACTCGGAGCGTGGACCT 1506
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604 TCCTGCGAGCCCACTCGGAGCGTGGAACT 631
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RESULT 9
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LOCUS 602659504F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802713 5',
DEFINITION mRNA sequence.
ACCESSION BG696408
VERSION BG696408.1 GI:13961522
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10697 row: g column: 02
High quality sequence stop: 707.
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 27.0%; Score 594; DB 12; Length 935;
Best Local Similarity 86.8%; Pred. No. 2.4e-108;
Matches 799; Conservative 0; Mismatches 65; Indels 56; Gaps 11;

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1062 GGCTTCTGAGTCCCGCATCTGCTTCTTAGAGGTATCTGGAGCAACCTGTATGACGCA 1121
 1 GGCTTCTGAGTCCCGCATCTGCTTCTTAGAGGTATCTGGAGCAACCTGTATGACGCA 60
 1122 ACTTCAGACAGCTTATCTAGGCTCTAGAGCCAGCAGTCTGGAGCCGTGGGTCA 1181
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 1182 GGAAACAGCCCACTTGAAGGAGGAGGCTCCCTCTGGAAGATAGAGAACACCTCT 1241
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 1242 CAACAGCCGAGATAGTGTAGTTTTCACGATCTTCTGAGCGTGGCTTCCACTGGCCC 1301
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 1302 AGGCCACACATATTTCTGCTGGCTCCATTTCCAAAGAGCTACTTTGAGCATCTTC 1361
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 1422 AGCCCACTGCTGCTGTGATGTGGTACCTCATCAATACAGCTGCTGCCCTTCC 1481
 361 AGCCCACTGCTGCTGTGATGTGGTACCTCATCAATACAGCTGCTGCCCTTCC 420
 1482 TGCAGCCCACTCGGAGCTGACCTCATCTGATGGGTCCCAACAGCTGACACCTCTGG 1541
 421 TGCAGCCCACTCGGAGCTGACCTCATCTGATGGGTCCCAACAGCTGACACCTCTGG 480
 1542 TCCAGAGTGTGAGCTCTGCTGGCGGTTCTGCGAGGAGCGGGATCCGTTCCCAACCA 1601
 481 TCCAGAGTGTGAGCTCTGCTGGCGGTTCTGCGAGGAGCGGGATCCGTTCCCAACCA 540
 1602 TCTGCCAGCCCGGAGAGAGAGCAGC-TCAGGCTGGG-AGTGCCACACCTT--CTCGAC 1657
 541 TCTGCCAGCCCGGAGAGAGAGCAGC-TCAGGCTGGG-AGTGCCACACCTT--CTCGAC 600
 1658 CCCACTGCCCCGAGCCCTCGGCTGCTGACATTTTCTC-----1698
 601 ACCAACTGCCCGAGCCCTGAGGTGCTGACATTTTCTC-----1698
 1699 -----TGGGCTCGGCGACACCCGAGGAGCGGCGAGCTG-GGGAGGT 1740
 661 GGAGTACTCGGACCCCATGGGTCGGCGGACACCCGAGGAGCGGCGAGCTGAGGGAGT 720
 1741 GAACCTG---TCTTCATGGAATCTCCCTACCACTA--CAGGAAGGTGACCTACAGCAG 1795
 721 GAACCTGGAATCCATACGAGATCTCCCTACCAATAGCAGGAAGGTGACCTACAGCAG 780
 1796 GAGGAGCTGGACAG---CTGCTGACCTGACACATTTACAT--CTCTGCAACACACAGGA 1851
 781 GAGGAGCTGGACAG---CTGCTGACCTGACACATTTACAT--CTCTGCAACACACAGGA 840
 1852 GAGGAGCTGGACAG---CTGCTGACCTGACACATTTACAT--CTCTGCAACACACAGGA 1905
 841 AGACACGCTGATGGAGGGAATGAGCCAGGAGGGAACAGAGGAGGAGGAGGAGGAGG 900
 1906 CCATGATGCGCGGCGCCC 1925
 901 ACATAGAAATGGCGAGGCCC 920

BM906397 1149 bp mRNA linear EST 12-MAR-2002
 AGENCOURT_6620095 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590352
 5', mRNA sequence.
 BM906397
 BM906397.1 GI:19356776
 EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1149)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12364 row: i column: 09
 High quality sequence stop: 568.

FEATURES
 Location/Qualifiers
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 /clone_lib="NIH_MGC_125"
 /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
 Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
 of three ovaries, from females ranging in age from 38 to
 49 yo. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 2.1 kb, insert size range 1-3.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 036."

ORIGIN
 Query Match 26.1%; Score 574.4; DB 12; Length 1149;
 Best Local Similarity 92.0%; Pred. No. 2e-104;
 Matches 653; Conservative 0; Mismatches 21; Indels 36; Gaps 3;
 QY 1492 TCAGGAGCTGACCTCATCTGCTGATGGATCACTCCAGGAGCGGGATCCCGTTCCACCCATCTCGCCAG 1551
 Db 11 TCAGGAGCTGACCTCATCTGCTGATGGATCACTCCAGGAGCGGGATCCCGTTCCACCCATCTCGCCAG 70
 QY 1552 GCAGCTCTGCGGCGGTTCTGCCAGGAGCGGGATCCCGTTCCACCCATCTCGCCAG 1611
 Db 71 GCAGCTCTGCGGCGGTTCTGCCAGGAGCGGGATCCCGTTCCACCCATCTCGCCAG 130
 QY 1612 CCCGAGAGAGAGCTCAGGCTCGGGAGTGCCACCTTCTCCGAGCCCACTGCCCCGG 1671
 Db 131 CCCGAGAGAGAGCTCAGGCTCGGGAGTGCCACCTTCTCCGAGCCCACTGCCCCGG 190
 QY 1672 AGCCCTCTGCGGCTGCTGACCTT-----TCTC 1698
 Db 191 AGCCCTCTGCGGCTGCTGACCTTCTCTGTGAGCGACTCTTCCGGAGTACTCGGCC 250
 QY 1699 TGGGCTCCGCGGACACCCGAGGAGCGGCGAGCTGGGAGGTGAACCTGCTTCATCGGA 1758
 Db 251 TGGGCTCCGCGGACACCCGAGGAGCGGCGAGCTGGGAGGTGAACCTGCTTCATCGGA 310
 QY 1759 CTCTCCCTACCTACACGAGGTGACCTACAGCCAGGAGCGTGGACAAAGTGTGTGCA 1818
 Db 311 CTCTCCCTACCTACACGAGGTGACCTACAGCCAGGAGCGTGGACAAAGTGTGTGCA 370
 QY 1819 CTGACACATTAATGCTGCAACACAGGAGCGAGCTGCTGGAGGCTTCGCCAGGC 1878
 Db 371 CTGACACATTAATGCTGCAACACAGGAGCGAGCTGCTGGAGGCTTCGCCAGGC 430
 QY 1879 AGTGAGCGGAGCGGCGAGCGAGGCGCCCACTGATGCGGGGCGCCCTGCGACCCCTAAC 1938
 Db 431 AGTGAGCGGAGCGGCGAGCGGCGCCCACTGATGCGGGGCGCCCTGCGACCCCTAAC 490

TITLE
JOURNAL
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD
cDNA Library Preparation: ResGen, Invitrogen Corp
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13739 row: g column: 15
High quality sequence stop: 622.

FEATURES
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/db_xref="taxon:10090"
/clone="IMAGE:631298"
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/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
Site 1: BcoRV; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 2.2 kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 25.5%; Score 562; DB 13; Length 922;
Best Local Similarity 83.6%; Pred. No. 6.2e-102;
Matches 637; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 610 CACCTGGGCTTGGCCAACTTTATGAGCACCAGAGTGTCTCAGAAGGACCTGGCAGG 669
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Db 2 CACAGAAGACCTGGCCAACTCTATGAGCACCAGAGTGTCTGCGAGAAGACCTGGCAGG 61
QY 670 GCCCTAGTGTCTGAAGACCCAGGTGACCAAGAACAAAGCTGGGTGTCTGGCCCCCAG 729
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Db 62 GCCCTAGTGTCTGAAGACACAGGTGACCAAGAACAAAGCTGGGTGTCTGGCCCCCAG 121
QY 730 CCAGCTGACGCGTACCGGACGAGCTGGCCGAGCTGCCCTGGGCTACCAAGCTG 789
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QY 790 CTTACCAACCTTGGGCGCTCATCAACGAGCGCTGTCTGATGATGAGCCCCCATGATCA 849
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Db 182 CTTACCAACCTTGGGCGCTCATTAATGAGCGCTTGTCTGACGACAGCCCCCATGAACA 241
QY 850 CAAGCTCTCAGATCAACGGGAGGCGCTGATGATGCGCCAGAACCTCTGCGCCATCTACTG 909
|||
Db 242 CAAGCTCTCAGATCAACGAGAGGCGCTGATGATGCGCCAGAACCTCTGCGCCATCTACTG 301
QY 910 TGCCCTCAACACCAAGGCGCAGAGCTGACCACTTTTGAATTTGGGAGTGGTGGAGTT 969
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Db 302 TGCCCTCAACAGCAGAGAGGCGCTGATGATGCGCCAGAACCTCTGCGCCATCTACTG 361
QY 970 CTCTCCCTACAGGTGGCTTCCCAAGTACGGGCGCTTATCCCTCTGAGCTCTTTGG 1029
|||
Db 362 CTCTCCATATGAAGTGGCTTCCCAAGTATGAGCGCTTATCCCTCTGAGCTCTTTGG 421
QY 1030 CTCCGAGTCTTTATGGGCGAGCTGATGAAGAGGCTTCTGAGTCCCGCATCTGCTTT 1089
|||
Db 422 CTCCGAGTCTTTATGGGCGGCGTGGTGAAGCAGCTTCCCGAGTCCCGCATCTGCTTCT 481
QY 1090 AGAAGGTATCTGAGCAACCTGTATGACGCAACCTCCAGACAGCTTATATCTGGGCTC 1149
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Db 482 GGAAGGATCTGGAGCAATCTGTTTGGCGGCGAGCTCCAGACAGCTTGTACTGGTCTC 541
QY 1150 AGAGCCAGCAGTTCTGGGACCGCTGGGTGAGAACCGAGCCCAACCTGGACAAAGGAGCA 1209
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Db 542 AGAAGCCAGCAGTTCTGGGACCGCTGGGCGCAGGATCAGGCGCAACCTGGACAAAGAGCA 601
QY 1210 GGTCCCCCTTCTGAGATAGAGAACCAACCTCAACAGCGGCGAGATAGCTGAGTTT 1269
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Db 602 GGTCCCCCTTCTGAGATAGAGAACCAACCTCAACAGCTCTCAACTCTC 763
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QY 1270 CACGATCTTCTGACGTGGCGTCCACTGGCCAGGCCACACATATTTCTGCGTGGCT 1329
|||
Db 662 CACTGAGCTCTGACAAAGCGTCCCTCGCCAGCCACCACTTCAGCGAGGCT 721
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QY 1330 CCATTTCACAAAGACTACTTTGAGCATCTCTACTTCTCCAC 1371
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Db 722 CCATTTCACAAAGACTATTTTCAGAAACTCTCAACTCTC 763
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RESULT 13
AW959903
LOCUS
DEFINITION
AW959903
ACCESSION
VERSION
AW959903.1
KEYWORDS
EST.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 666)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
CONTACT: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 139
Seq primer: Reverse.
Location/Qualifiers
1. .666
/organism="Homo sapiens"
/mol_type="mRNA"
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/note="Vector: pBluescriptSKm"

ORIGIN

Query Match 25.3%; Score 558.2; DB 10; Length 666;
Best Local Similarity 92.0%; Pred. No. 3.6e-101;
Matches 612; Conservative 0; Mismatches 20; Indels 33; Gaps 1;

QY 1275 ATCTTCTGACGTGGCGTCCACTGGCCAGGCCACACATAATTTCTGCGTGGCTTCCATT 1334
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Db 1 ATCTTCTGACGTGGCGTCCACTGGCCAGGCCACACATAATTTCTGCGTGGCTTCCATT 60
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QY 1335 TCCCAAGAGACTATTTGAGCATCTCTACTTCTCAATGAAAGCTACCACTCTGGATG 1394
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Db 61 TCCCAAGAGACTATTTGAGCATCTCTACTTCTCAATGAAAGCTACCACTCTGGATG 120
|||
QY 1395 GGCTCCCCCAACAGCTGACACCCCTCGGAGCCCACTGTGCTGCTGATGTTGGCTACC 1454
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Db 121 GGCTCCCCCAACAGCTGACACCCCTCGGAGCCCACTGTGCTGCTGATGTTGGCTACC 180
|||
QY 1455 TCATCAATACAGTGGCTGCCCTCTCTGAGCCCACTCGGAGAGCTGACCTCATCTGT 1514
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Db 181 TCATCAATACAGTGGCTGCCCTCTCTGAGCCCACTCGGAGAGCTGACCTCATCTGT 240
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|||
QY 1575 AGGAGCAGGGGATCCCGTCTCCCACTCTCGCCAGCCCGGAGAGACACTCAGGCTC 1634
|||

301 AGGAGCAGGGGATCCCGTTCCACCATCTCGCCAGCCCGGAGAGCAGCTCCAGCCCTC 360
 1635 GGGAGTGCACACCTTCTCGGACCCACCTGCGCCCGGAGCCCTCGGCTGCTGCTGCTTT 1694
 361 GGGAGTGCACACCTTCTCGGACCCACCTGCGCCCGGAGCCCTCGGCTGCTGCTGCTTT 420
 1695 C-----CTCTGGGGTCCGGCGGACACCCGAGG 1721
 421 CTCTGGTACGCGACTCTTTCGCGAGTACTCGGCGCCCTTGGTCCGCGGACACCCGAGG 480
 1722 AGGCGGAGCTGGGAGGTGAACCTGCTTTCATCGGACTCTCCCTACCACTACACGAAGG 1781
 481 AGGCGGAGCTGGGAGGTGAACCTGCTTTCATCGGACTCTCCCTACCACTACACGAAGG 540
 1782 TGACCTACAGCCAGGAGGAGCTGACCAAGCTGCTGACCTGACCATTAATGCTTGCA 1841
 541 TGACCTACAGCCAGGAGGAGCTGACCAAGCTGCTGACCTGACCATTAATGCTTGCG 600
 1842 ACACACGAGGAGCAGCTGCTGAGGCTCTGCGCCAGGAGTGCAGCGGAGGCGGAGGCGCA 1901
 601 ACACACGAGGAGCAGCTGCTGAGGCTCTGCGCCAGGAGTGCAGCGGAGGCGGAGGCGCA 660
 1902 GGCCC 1906
 661 GGCCC 665

CA319426 810 bp mRNA linear EST 09-JUL-2003
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 IMAGE:6816688 5', mRNA sequence.
 CA319426
 CA319426.1 GI:24537550
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 810)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.
 Location/Qualifiers
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 Site 2: Not I; The library was constructed according
 Bonaudo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated

with Ecor I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGGAGACAG. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN
 Query Match 25.2%; Score 556.2; DB 14; Length 810;
 Best Local Similarity 82.4%; Pred. No. 9e-101;
 Matches 672; Conservative 0; Mismatches 138; Indels 6; Gaps 3;
 QY 709 GCTGGGGTGTCTGGCCCGCCAGCAGCTGCAGCGGTACCGGAGGAGTGGCCGAGCGTGC 768
 Db 1 GCTGGGTGCTGGCCCGCCAGCAGCTGGCGGTACCGGAGGAGTGGCGTGCAGCGTGC 60
 QY 769 CGGCTTGGGTACCCAGCTGCTTCAACACCTTGGGCGCTCATCAACGAGGCGCTGCT 828
 Db 61 TCGCTTGGGCGACCCAGCTGCTTCAACAACTTGGGCGCTCATTAATGAGGCGCTTGTCT 120
 QY 829 GCATGATGAGCCCATGATCACAGCTCTCAGATCAACGAGGAGGCGCTTGAATGAGCGCA 888
 Db 121 GCAGCAGAGCCCATGAAACAACTCTCAGATCAACGAGGAGGCGCTTGAATGAGCGCA 180
 QY 889 GAACCTCTGCGCCATCTACTGTGCGCTCAACACAAAGGAGGAGGCGCTTGAATGAGCGCA 948
 Db 181 GAACCTCTGCGCTATCTATGTCCTCAACAGAGGAGGAGGCGCTTGAATGAGCGCA 240
 QY 949 ATTTGGGAGTGGTGGAGTCTCTCCCTAGAGTGGGCTTCCCAAGTACGGGCGCTT 1008
 Db 241 CTTTGGGAGTGGTGGAGTCTCTCCATATGAAGTGGGCTTCCCAAGTATGGAGCGCTT 300
 QY 1009 CATCCCTCTGAGCTCTTTGGCTCGAGTCTTTATGGGCGAGCTGATGAAGAGCTTCC 1068
 Db 301 CATCTCTCCAGCTCTTTGGCTCGAGTCTTTATGGGCGGCTTGAAGAGCTTCC 360
 QY 1069 TGAGTCCCGCATCTGCTTCTTTAGAGGATCTGGAGAACCTGTATGAGCGCAACTGCA 1128
 Db 361 CGAGTCCCGCATCTGCTTCTTGAAGGATCTGGAGCAATCTGTTGGGCGGAGCTTCCA 420
 QY 1129 GGACAGCTTATCTGGGCGCTGAGCCCGAGCGCTTCTGGGACCGCTGGGTGAGGAGCA 1188
 Db 421 AGACAGCTTGTACTGGTCTCTCAGAACCCAGCGAGTCTGGGAGCGCTTGGGCGGAGCA 480
 QY 1189 GGCCAACTGGACAGGAGCAGTCCCTCTCTGAAGATAGAAGAACCACTCCCTCAACAGC 1248
 Db 481 GGCCAACTGGACAGGAGCAGTCCCTCTCTGAAGATAGAAGAACCACTCCCTCAACAGC 540
 QY 1249 CGGCAAGATAGCTGAGTCTTTTACCGATCTTCTGACGCTGCGGCGTCCACTGGGCGG 1308
 Db 541 TGGCAGGATCGCGAGCTCTTCACTGAGCTCTGACAAAGCGTCCCTGCGCCAGCGCAC 600
 QY 1309 ACATTAATTTCTGGGCGCTCCATTTCCACAAGACTACTTTCCAGACTCTTCACTTCTC 1368
 Db 601 CCACAACCTTACGCGAGGCGCTCCATTTCCACAAGACTATTTCCAGAACTCTCACTTCTC 660
 QY 1369 CACATGGAAGAGCTACCACTCTCGATGGGCTCCCGAACCACTGACACCTCTGGAGCGCA 1428
 Db 661 TGCCTGGAAGAGCTTCCAACTTGAAGAGCTTCCCGAACCACTGAGCA-CCACTGAGCGCA 719
 QY 1429 CTTGTGCTTGTGATGTTGGTACTCATCAATACAGCTGCTGCTGCGGCTTCTGAGCGC 1488
 Db 720 CTTGTGCTTGTGATGTTGGTACTCATCAATACAGCTGCTGCTGCGGCTTCTGAGCGC 777
 QY 1489 CACTCGGAGCTGGAGCTCATCTGCTGCTTGGACTA 1524
 Db 778 CAC---GGGATGTGAGTCACTTGTGACTTGGACTA 810

RESULT 15
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